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Result
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2004 Compugen Ltd.
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p37709 oryctolagus
p08799 dictyosteli
Q28641 oryctolagus
p08799 dictyosteli
Q28641 oryctolagus
Q07283 homo sapien
Q9ukx3 homo sapien
Q9ugs7 homo sapien
Q9ugs7 homo sapien
Q12824 homo sapien
p12886 homo sapien
p12886 saccharomyc
Q5598 mus musculu
p12844 caenorhabdi
Q02455 saccharomyc
Q59996 h a-kinase
p29616 gallus gall
p35749 homo sapien
p22793 ovis aries
Q9u6a1 drosophila
p12543 rattus norv
Q13439 homo sapien
Q15643 pallus gall
Q9ukx2 homo sapien
p10587 gallus gall
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O9ptd7 xenopus lae
P59242 mus musculu
O9uif8 homo sapien
O9p2m7 homo sapien
P13535 homo sapien
O67124 aquifex aeo
P02562 oryctolagus
O9h266 homo sapien
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I	MYH3 CHICK	MYH6 HUMAN	RASO_THEMA	SPCO MOUSE	MYHB RABIT	YAFA SCHPO	CF60 HUMAN	REST HUMAN	SMC_METJA	PEPL_MOUSE	SCP1_HUMAN	MYHB_MOUSE
		P13533 homo sapien	Q9x1x1 thermotoga		P35748 oryctolagus	_		•••	_	_		

ALIGNMENTS

DR DR DR DR R DR R DR R DR R DR R DR R	ននននននន	000000000000000000000000000000000000000	RESULT BA2B CC AC OC
EMBL; AF224275; AAG36791.1; HSSP; Q92831; 1B91. InterPro; IPR001487; Bromodomain. InterPro; IPR001487; Methyl-CpG_bind. InterPro; IPR001739; Methyl-CpG_bind. InterPro; IPR001965; Znf_pHD. Pfam; PF00439; bromodomain; 1. Pfam; PF00439; bromodomain; 1. Pfam; PF00429; MBD; 1. Pfam; PF00429; MBD; 1. PFAMT; SM00297; BROMODOMAIN. SMART; SM00297; BROMODOMAIN. SMART; SM00297; BROMODOMAIN. SMART; SM00249; PHD; 1. SMART; SM00249; PHD; 1. PROSITE; PS00633; BROMODOMAIN_1; FALSE NEG. PROSITE; PS0063; BROMODOMAIN_2; 1. PROSITE; PS001359; ZF PHD 1; FALSE NEG. PROSITE; PS001359; ZF PHD 1; FALSE NEG. PROSITE; PS0016; ZF PHD 2; 1. Transcription regulation; Bromodomain; Zinc-finger; Coiled coil; Nuclear protein; DNA-binding.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	GALLUS. (CBI_TaxID=9031; (1) (1) SEQUENCE FROM N.A. SEQUENCE FROM N.A.; YOON H. Philp N.J.; YOON H. Philp N.J.; YOON H. Philp N.J.; YOON H. Philp N.J.; SUBMITTED OF a new extracellular matrix protein expressed in retina."; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. -!- FUNCTION: May play a role in transcriptional regulation. -!- SIMILARITY: Belongs to the WAL family. -!- SIMILARITY: Contains 1 bromodomain. -!- SIMILARITY: Contains 1 DDT domain. -!- SIMILARITY: Contains 1 PHD-type zinc finger.	1 1

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RT cultured cells.", 17:27757-27764 (2002).

REL J. Biol. Chem. 277:27757-27764 (2002).

CC - i- FUNCTION. Probably plays a role in the formation and regulation of the tight junction (TJ) paracellular permeability barrier, the tight junction (TJ) paracellular permeability barrier.

CC - i- SUBUNIT: Parallel homodimer (By similarity). Binds ZO-1 and ZO-2 CC - in vivo, and ZO-3, myosin and occludin in vitro, possibly in vivo, and ZO-3, myosin and occludin in vitro, consisting the cc. in vivo, and ZO-3, myosin and sociation in vitro, directly. Acts as an F-actin bundling protein in vitro consisted cc. i- ISSUB SPECIFICITY: Localized on the cytoplasmic face of tight cc. junctions of polarized epithelia and some endothelia.

CC - i- TISSUB SPECIFICITY: Localized constant some endothelia.

CC - i- DEVELOPMENTAL STAGE: A maternally synthesized protein. Found in CC constitution of the fortilized egg, where it is associated with cytoskeleton filaments, it is recruited to tight junctions cc. with cytoskeleton filaments, it is recruited to tight junctions before ZO-1 and occludin. Nascent tight junctions are in place before ZO-1 and occludin. Nascent tight junctions are in place before ZO-1 and occludin. Nascent tight junctions are in place before ZO-1 and occludin. Nascent tight junctions are in place before ZO-1 and occludin in the raction motif (ZIM) decreases but cc. - i- DOMAIN: Deletion of the ZO-1 interaction motif (ZIM) decreases but cc.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-OCT-2003 (Rel. 42, Last annotation update) Cingulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cordenonsi M., D'Atri
Shore D., Citi S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Oocyte;
MEDLINE=20082893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION IN TIGHT JUNCTION BIOGENESIS. MEDLINE=20400099; PubMed=10940624; Fesenko I., Kurth T., Sheth B., Fleming "Tight junction biogenesis in the early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cardellini P., Davanzo G., Citi S.;
"Tight junctions in early amphibian development: detection of junctional cingulin from the 2-cell stage and its localization at the boundary of distinct membrane domains in dividing blastomeres in low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION IN TIGHT JUNCTION BIOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cordenonsi M., Turco F., D'Atri F., Hammar E., Martinucci G., Cordenonsi M., Turco F., D'Atri F., Hammar E., Martinucci G., Meggio F., Citi S.;
Meggio F., Citi S.;
"Xenopus laevis occludin. Identification of in vitro phosphorylation "Xenopus laevis occludin. Identification of in vitro phosphorylation sites by protein kinase CK2 and association with cingulin.";
Sur. J. Biochem. 264:374-384(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     calcium.";
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MEDLINE=21538627; PubMed=11682052;
D'Atri F., Citi S.;
"Cingulin interacts with F-actin i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mech. Dev. 96:51-65(2000).
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Cordenonsi M., Turco F., D'Atri F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22140336; PubMed=12023291;
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s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
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GO:0003779; F:actin binding; IDA.
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HEEIFDLEKE
                                                                    VVGQQQQNINPSSNDDCRKRAEEVSSFIEFQEKEMEEFVEEREMLIKDQEKKMEDMKKRH
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                                   LKGTLKEEVSGRDRETVRLR-EQLQSEVMHVKKENEGLAKESRR-IQDQLKQVLLEKQRH
                                                                                                        SLLQSELAQVKKGSVDPGEVASVRKELQRVQDQLKQLSVDKQKVEEN--
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Pred. No. 0.
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INTERACTS WITH ZO-2.
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RX Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschal S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschal S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Pahey J., Helton E., Ketteman M., Madan A., Gay L.J., Hulyk S.W.,

RA Pahey J., Helton E., Ketteman M., Madan A., Godrigues S., Sanchez A.,

RA Rodriguez A.C., Schein J.W., Green E.J., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Rodriguez A.C., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

"Generation and mouse cDWA sequences"."

"Generation and mouse cDWA sequences"."

"Generation and mouse cDWA sequences "By 16899-16903 (2002).

--- FUNCTION: Probably plays a role in the formation and regulation of

the tight junction (TJ) paracellular permeability barrier (By

"Generation and paracellular permeability barrier (By
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003
10-OCT-2003
                                                                                                                                                                                                                                                                      GO; GO:0005923; C:tight junction; NAS GO; GO:0003779; F:actin binding; ISS.
                                                                                                                                                                                                                                                                                                                                EMBL; BC042459; AAH42459.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cingulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P59242;
                                                                                                                                                                                                                             InterPro; IPR002928; Myosin_tail.
Pfam; PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Homodimer. Interacts with TJP1/ZO-1 (By similarity) DOMAIN: Deletion of the ZO-1 interaction motif (ZIM) decreas does not abolish colocalization with ZO-1 (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
                                                                                                                                                                                                                                                                                                               MGI:1927237; Cgn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOUSE
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                                                                                                                                                                                      junction;
                     similarity 18.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EETVHORERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lus (Mouse).
; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                  343
1149
357
42
1191
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(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                           Coiled coil.
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                                                                                  136446
                                                                                  MW;
                                                                                                   GLU-RICH.
ZIM.
                                                                                                                                            HEAD.
COILED
TAIL.
                     Score 183; DB 1; Length 1191; Pred. No. 0.025;
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                                                                                  43EA20F49AF5E7D9
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BA2B HUMAN
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AC Q9UIF8
DT 28-FEB
DT 28-FEB
DT 15-MAR
DE Bromod

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-AA2B HUMAN STANDARD; PRT; 1972 AA
O9UIFB; Q96EA1; Q96SQ8; Q99252; Q9Y4N8;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation updat
Bromodomain adjacent to zinc finger domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V$QN$NPPRAWGGQQQGRGSNVSGRGNNVSGRGNGRGI----QANISG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSGRRPARDARASTYGVAVRVQGIAGQPFVVLNSGEKGTDSFGVQIKGGNNRGSPGA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FGSLDS-----LSIEQINEP------QRQWHCPACQNGPGAIDWY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       relaemgldriamgoxrsmfsggvrolygflatkodldifnohsogktrlkfelksyoem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GMGNQELLEYFDKYEALRARHSYG-PQGHRGMSVLMFESSATGYLEAER------LH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ROKLEPSRVGLERQLEEKAEECHRLQELLERRKGEVOOSSKELQNMKLLLGQEEGLRHGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WYKELROI---SEDNOOLNYFKNKL-----SKONKHA-----KVLEESLEIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REEADRGRELEQQNLQLQKTLQQLRQDCEEASKAKVASETEAMMLGQRRATVETTLRETQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEKL--RRTAEDNRIVRORTKMOHEON------REEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQRDLEQARASTRDTHQVEELKKELRRTQGELKELQAEQQNQEVTGRHRNQVLEKQLAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAHDRF---
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                                                                                                                                                                                                                 901
                                                                                                                                                                                                                                                          625
                                                                                                                                                                                                                                                                                                                                   -KEMEEFVEEREMLIKDQEKKMEDMKKRHHEEIFDLEKEF-DEALEQLMYKHGLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LEKDLOMRGASVIPCGEIYGQWKG------LGEDE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----veqlvqglagtr--lassqddggeweviskknknkpgntsgktw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -LAPKPTSSINTIDTAPLSSVDSLINKFDSQKGG---QVRGRTGRRT--R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - OSMFOKNKEEL - - - RATKOEL - - - LOLRMEKEEMEEELGEKMEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---NLHPL--LAHARTKG-ARRVKLHRELAEV-----
                                                                                                                                                                                                                                                                                                                                                                                                                             -GOOOONINPSSNDDCRKRAEEVSSFIEFOE
        ion update)
c domain 2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----FMDSIKQIHERRDAKEENFEMLQQQE-
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               (hWALp4).
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                          RX MEDLINE=2238825/; Pubmeu=144/7326

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RS Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,

RA Hausner R.D., Colline F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Joshiyuki S., Carninci P., Hl.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Bakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Bakesley R.W., Touchman J.W., Mara M.A.,

"Generation and initial analysis of more than 15,000 full-length

"Generation and mouse cDNA sequences",

"Generation and mouse cDNA sequences",

"Generation and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20277482; PubMed=10819331;
Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes.
The complete sequences of 100 new cDNA clones from brain which co
for large proteins in vitro.";
DNA Res. 7:143-150(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BAZ2B OR KIAA1476
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Ohara O., Nagase T.,
Submitted (APR-2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jones M.H., Hamana N., Nezu J., Shimane "A novel family of bromodomain genes."; Genomics 63:40-45(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20130112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-776 FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-799 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Melanoma
                                                                                                                                                                                                                                                                                             Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki Y., Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Kanehori K.;
                                                                                                                                                       Submitted (JUN-1999)
                                                                                                                                                                                                  TISSUE=Testis;
                                                                                                                                                                                                                 SEQUENCE OF 1524-1972
                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                  "NEDO human
                                              stka A., Klein M., Mewes H.-W., Gassenhuber J., Wien mitted (JUN-1999) to the EMBL/GenBank/DDBJ databases FUNCTION: May play a role in transcriptional regulainteracting with ISWI.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Comment=Experimental confirmation may be lacking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (JUL-2002) to
                                                                                                                                                                                                                                                              n cDNA sequencing (MAY-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                    F 427-1215 FROM N.A. (ISOFORM 3).
Ota T., Hayashi K., Sugiyama T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=10662543;
a N., Nezu J., Shimane M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ISOFORM
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                                                                                                                                                                                                                          FROM
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the EMBL/GenBank/DDBJ

    3).
    R.;
    EMBL/GenBank/DDBJ

                                                                                                                                                                                                                          N.A.
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EMBL/GenBank/DDBJ
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databases.
                                                                                                                                                                r J., Wiemann
databases.
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PRINTS; PRO0563; BROMODOMAIN.
SMART; SM00297; BROMO; 1.
SMART; SM00297; BROMO; 1.
SMART; SM00291; MBD; 1.
SMART; SM00214; MBD; 1.
SMART; SM00249; PHD; 1.
SMART; SM00249; PHD; 1.
PROSITE; PS00633; BROMODOMAIN_1; FALSE_NEG.
PROSITE; PS0014; BROMODOMAIN_2; 1.
PROSITE; PS0104; BROMODOMAIN_2; 1.
PROSITE; PS01015; ZF_PHD 1; FALSE_NEG.
PROSITE; PS01015; ZF_PHD 2; 1.
Transcription_regulation; Bromodomain; Zinc-f.
                                                                                                                                                                                                                                                                                                            Pfam; PF02791;
Pfam; PF01429;
Pfam; PF00628;
                                           ZN FING
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                     MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AK027612; BAB55231.1;
EMBL; AL080173; CAB45759.1;
PIR; T12495; T12495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB040909; BAA96000.2;
EMBL; AL834381; CAD39044.1;
EMBL; BC012576; AAH12576.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                            Pfam; PF00439;
                                                                                                                                                                             Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; Q92831;
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                                                                                                                                                      DOMAIN
                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                   InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                         interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: Belongs to the WAL family.

SIMILARITY: Contains 1 bromodomain.

SIMILARITY: Contains 1 DDT domain.

SIMILARITY: Contains 1 methyl-binding (MBD) domain.

SIMILARITY: Contains 1 PHD-type zinc finger.

CAUTION: Ref.5 sequence differs from that shown due
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q9UIF8-3; Sequence=VSP_000554;
Note=Inferred from Ref.5;
TISSUE SPECIFICITY: Expressed at varying levels in several tissues, whereas a smaller transcript was expressed specif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             frameshift in position 731.
                                                                                                                                                                                                                                                                                                                                                                                                     605683;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=Q9UIF8-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q9UIF8-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                            HGNC:963; BAZ2B.
                                                                                                                                                                          protein;
                                                                                                                                                                                                                                                                                                                                                       IPR004022; DDT_dom.
IPR001739; Methyl-CpG_bind
IPR001965; Znf_PHD.
                                                                                                                                                                                                                                                                                                                                                                                      IPR001487; Bromodomain.
                                                                                                           891
1735
1881
45
73
                                                                                                                                                                                                                                                                                                            ; bromodomain;
; DDT; 1.
; MBD; 1.
; PHD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         1891
                                                                                                                                                                          DNA-binding;
                                           956
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1951
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470
672
865
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rom Ref.4;
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4.1; ALT_INIT.
6.1; ALT_FRAME.
1.1; ALT_INIT.
                                                                                                                                                                                     Bromodomain; Zinc-finger; Coiled
ASP-RICH.
COILED COIL (POTENTIAL).
Missing (in isoform 2).
/FTId=VSP_000553.
Missing (In isoform 3).
/FTId=VSP_000554.
                                                                         ARG-RICH.
COILED COIL (POTENTIAL).
                                                                                                 ASP/GLU-RICH
                                                                                                                       SER-RICH.
                                                                                                                                PHD-TYPE.
BROMODOMAIN.
                                                                  LYS-RICH.
                                                                                                            POLY-GLU
                                                                                                                                                                          Alternative splicing
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                                isoform 2).
                                            (POTENTIAL)
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DT CINGUI
GN CGN OR
OS HOMON
OS ENLARY
OC MARMAI
RP SEQUEN
RC TISSUE
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Query Match
Best Local
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28-FEB-2003 (Rel
28-FEB-2003 (Rel
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                                                 Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                         Cingulin.
CGN OR KIAA1319
SEQUENCE FROM N.A. TISSUE=Neuroepithelium;
                                     NCBI_TaxID=9606;
                                                                                                                      10-OCT-2003
                                                                                                                                                                        CING_HUMAN
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                                                                                                                                                                                                                                                                  MEDM 592
                                                                                                                                                                                                                                                                                                                  LQQQERAKVVGQQQQNINPSSNDDCRKRAEEVSSFIEFQEKEMEEFVEEREMLIKDQEKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VLMFESSA--TGYLEAERLHRELAEMGLDRIAWGQKRSMFSGGVRQLYGFLATKQDLDIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDDDKDQDESDSDTEGEKTSMKLNKTTSSVKSPSMSLTGHSTPRNLHIAKAPGSAPAALC
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                                                                                                                                                                                                                                                                                                                                                                                                  ----KRKQKEQIKIMKQQEKIKRIQQIRMEKELRAQQILEAKKKKKEEAANAKLLEAE
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                                        s (Human).

Metazoa; Chordata; C

Metazoa; Primates; (
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226
627
722
790
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(Rel. 41, Last sequence update)
(Rel. 42, Last annotation update)
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Pred. No. 0.
                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                        PRT;
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Best Local S
Matches 173
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Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O
"Prediction of the coding sequences of unidentified human
The complete sequences of 150 new cDNA clones from brain w
for large proteins in vitro.";
DNA Res. 7:65-73(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20499514; PubMed=11042084; Citi S., D'Atri F., Parry D.A.D.; "Human and Xenopus cingulin share a coiled-coil rod domain: predictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22140336; PubMed=12023291;
D'Atri F., Nadalutti F., Citi S.;
"Evidence for a functional interaction between cingulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      assembly.";
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Eor
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                                                                                                                                                                                                                                                                                                                                                                                                                                       the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
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J. Biol. Chem. 2
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                                                                                                                                                                                                                                                                                Tight
DOMAIN
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                                                                                                                                                                                                                                                                                                                      InterPro; IPR002928; Myosin_
Mam; PF01576; Myosin_tail;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Struct. Biol. 131:135-145(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUNCTION: Probably plays a role in the formation and regulation FUNCTION: Probably plays a role in the formation and regulation the tight junction (TJ) paracellular permeability barrier. SubuNIT: Homodimer (By similarity). Interacts with TJF1/ZO-1. SUBUNIT: Homodimer (By similarity). Interacts with TJF1/ZO-1. TISSUE SPECIFICITY: Localized on the cytoplasmic face of tight placetion of polarized epithelia and some endothelia. Expressed junctions of polarized epithelia and some endothelia. Expressed pancreas, kidney, liver and lung, but not in skeletal muscle, placenta, brain or heart.

DOMAIN: Deletion of the ZO-1 interaction motif (ZIM) decreases b does not abolish colocalization with ZO-1.
                                                                                                                                                                                                                                                                                                                                                 GO:0005923; C:tight junction; NAS:
GO:0003779; F:actin binding; ISS:
GO:0005515; F:protein binding; IPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                      AF263462; AAF74498.1; ALT_INIT.
AB037740; BAA92557.1; ALT_INIT.
; HGNC:17429; CGN.
                           120
                                                                                                                                                                                                                                                                                                           junction;
                                                                                                         31
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                                                                                                       RÖGRRÞAKDARASTYGVAVRVÓGTAGQÞFVVLNSGEKGGDSFGVQTKGANDQG-ASGA--
                                                                              V$QNSNPPRAWGGQQQGRGSNVSGRGNNVSGRGNGNGRGI----QANISGRGRALSRKYD
 NNFV-APPPVSRP-----PLE----
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363
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ZIM.
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Pred. No. 0.046;
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                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                     RACTS WITH ZO-2.
0C9375283ABAAF3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modular organization for intra- and interm
                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                ----GGWNWQARGGSAQHTAVQEFPDVE
                                                                                                                                                                      284;
                                                                                                                                                                                              1:
                                                                                                                                                                                            Length 1197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          zation of the intermolecular
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                                                                                                                                                                      332;
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MBL outstation -
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SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
TISSUE=Skeletal muscle;
MEDLINE=90323631; PubMed=2373371;
MEDLINE=90323611; PubMed=2373371;
Karsch-Mizrachi I., Feghali R., Showe
"Generation of a full-length human peencoding cDNA.";
                                                                                                                                        MYH8 HUMAN STANDARD, P13535; Q14910; P13535; Q14910; O1-JAN-1990 (Rel. 13, Created) O1-JAN-1998 (Rel. 36, Last sequence up 15-JUL-1998 (Rel. 43, Last annotation 15-MAR-2004 (Rel. 43, Last annotation skeletal muscle, F
                                                                                                                                                                                                                   HUMAN
                                                                                                                                     8HYM
                                                                                  NCBI_TaxID=9606;
                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                         Homo sapiens
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                                                                                                    Chordata;
Primates;
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Catarrhini;
                                     Shows
                       perinatal
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perinatal
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                                   H.B.
                                                                                                                   Vertebrata;
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                                                                                                        Hominidae;
                                   Jr.,
                          myosin
                                                                                                                                                       (MyHC-perinatal).
                                   Leinwand
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                            wand L.A.;
heavy-chain-
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MIM; 160741; -.

MIM; 160741; -.

GO; GO:0005859; C:muscle myosin; TAS.
GO; GO:0008307; F:structural constituent of
InterPro; IPR000048; IQ region.
InterPro; IPR001609; Myosin_N.

InterPro; IPR0014009; Myosin_tail.
                  Pfam; PF00612;
Pfam; PF00063;
Pfam; PF02736; 1
Pfam; PF01576; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Esser K., Tidhar A., Myszkowski M.;

"Isolation and characterization of the human perinatal MHC promoter.";

Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Muscle contraction.

-!- SUBUNIT: Muscle myosin is a hexameric protein that consists of 2 heavy chain subunits (MHC), 2 alkali light chain subunits (MLC) and 2 regulatory light chain subunits (MLC-2).

-!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-!- DOMAIN: The rodlike tail sequence is highly repetitive, showing cycles of a 28 residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils.
-!- MISCELLANEOUS: Each myosin heavy chain can be split into 1 light meromyosin (LMM) and 1 heavy meromyosin (HMM). It can later be
                                                                                                                                                                                                                           PIR; 138055; 138055.
HSSP; P13538; 2MYS.
                                                                                                                                                                                                                                                              EMBL; M36769; AAC17185.1; -.
EMBL; Z38133; CAA86293.1; -.
EMBL; X51592; CAA35941.1; -.
EMBL; AF067143; AAC21557.1;
                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95324556; PubMed=7601129;
Jullian E.H., Kelly A.M., Pompidou A.J., Hoffman R., Schiaffino Stedman H.H., Rubinstein N.A.;
"Characterization of a human perinatal myosin heavy-chain transcript.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             split further into 2 globular subfragments (S1) and 1 rod-shaped subfragment (S2).
-i- SIMILARITY: Contains 1 myosin-like globular head domain.
-i- SIMILARITY: Contains 1 IQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Feghali R., Leinwand L.A.;

"Molecular genetic characterization of a human perinatal myosin heavy chain.";

J. Cell Biol. 108:1791-1797(1989).
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TISSUE=Skeletal muscle;
                                                                                                                                                                                                              Genew; HGNC:7578; MYH8.
                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 860-1937 FROM N.A. MEDLINE=89234168; PubMed=2715179;
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Bober E., Buchberger-Seidl A., Braun T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 89:289-294(1990).
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arnold H.H.;
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 PR00193;
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                Myosin
                                                  myosin_head; 1.
                               Myosin_N;
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MYOS INHEAVY.
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NP_BIND
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Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; Myosin; Multigene family; Calmodulin-binding.
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SMART; SM00242; MYSC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                     HRELAEMGLDRIAWGQKRSMFSGGVRQL-----YGFLATKQDLDIFNQHSQGK-
                                                                             LKEQLAIVERRANLLQAEIEELWATLEQTERSRKIAEQELLDASERVQLLHTQNTSLINT
                                                                                                                                                     EDNRIVRORTKMOHEONREEMDAH--DRFFMDSIK------OIH-----
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  KKRHHEEI FDLEKEFDEALEQLMYKHG
                            KKKLENDVSQL---
                                                    CRKRAEEVSSFIEFQEKEMEEFVEE-----
                                                                                                                             SRNDALRVKKKMEGDLNEMEIQLNHANRLAAESLRNYRNTQGILKETQLHLDDALRGQED
                                                                                                                                                                               LRIQLELNQVKSEVDRKIAEKDEEIDQL-----KRN-HTRVVETMQSTLDAEIR---
                                                                                                                                                                                                       TRIKFELKSYQEMVVKELRQISEDNQQLNYFKNKLSKQNKHAKVLEESIEIMSEKLRRTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                    ----ERR----QNINPSSNDD
                                                                                                                                                                                                                                                                                                                                 -----LQEAEEHVEAVNAKCASLEKTKQRLQNEVEDLMLDVERSNAACAALDKK 1448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ĀĀ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            970
1072
1247
1252
1261
1261
1297
1378
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19.3%;
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680
774
132
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                           -QSEVEEVIQESRNAEEKAKKAITDAAMMAEELKKEQDTSAHLERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A -> R (IN REF. 2).

A -> R (IN REF. 1 AND 4).

M -> N (IN REF. 3).

N -> H (IN REF. 1 AND 4).

MC -> DGG (IN REF. 3).

E -> G (IN REF. 1 AND 4).

K -> Q (IN REF. 1 AND 4).

K -> Q (IN REF. 3).

XY -> NT (IN REF. 3).

EN -> AH (IN REF. 1 AND 4).

B -> D (IN REF. 1 AND 4).

B -> D (IN REF. 1 AND 4).

B -> D (IN REF. 1 AND 4).

B -> H (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                   -----RTKYETDAIQRTEELEEAKKKLAQR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW; A3EE2D151792E9E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 174; DB 1;
Pred. No. 0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIN-BINDING ACTIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHYLATION (TRI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COILED COIL (POTENTIAL)
   619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SKQASTQQIEELKHQLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                   --- REMLIKDQEKK--MEDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                            1785
                                                     592
                                                                                                                                                                                                                                 1561
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KKNLEQTVKDLQHRLDEA-EQLALKGG

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Best Local S
Matches 130
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067124;
16-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; Progaso; Dec. 1.
TIGREAMS; TIGRO6618; sbcc; 1.
DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete proteome.
DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete proteome.
DNA repair; Hydrolase; ATP-binding; Coiled Coil; Complete proteome.

ATP-DIMENSITY OF STATE O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98196666; PubMed=9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
Deckert G., Warren P.V., Gasterland T., Young W.G., Lenox A.L.,
Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aquifex aeolicus.
Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probable DNA doubl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQUAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMAP; MF_00449; -; 1.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR007523; DUF498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 392:353-358(1998).

-- FUNCTION: Involved in DNA double-strand break repair (DSBR). The rad50/mrell complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease activity.

Rad50 provides an ATP-dependent control of mrell by unwinding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=VF5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A70387; A70387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE000718; AAC07092.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Belongs to the SMC family. RAD50 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aeolicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
18-FEB-2003 (Rel. 41, Last annotation update)
Probable DNA double-strand break repair rad50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF04430; DUF498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and/or repositioning DNA ends into the mrell active
                                    236
                                                                                              286 IDKKLTELKVRKNKLTKELAVLKDELSFAQEELNRIEAEKEKFKEEKEREKE------
                                                                                                                                                                                                                                                                                                                                                                                        106 NISGRGRALSRKYD--NNFVAPPPVSRPPLEGGWNWQARGGSAQHTAVQEFPDVEDDVDN 163
                                                                                                                                                                                                                        226 LRQELKKAEEKDSLERELSQVVTKLKELENLEKEVEKLREKLEFSRKVAPYVPIAKRIEE 285
                                                                                                                                                                                                                                                                                      164 ASEEENDSDALDDSDDDLAS-----DDYDSDVS---QKSHGSRK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
GAIDWYNLHPLLAHARTKGARRVKLHRELAEVLEKDLQMRGASVIPCGEIYGQWKGLGED 295
                                                                                                                                                                                                                                                                                                                                                       NLEGKREALKKEYELLKDYT---PTKKEVLE-----KTLKNLEEELKELKETEEK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR004592; SbcC.
IPR002017; Spectrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Forms a complex with mrell (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                         QNKWFKKFFGSLDSLSI--EQIN-----EPQRQWHCPACQNGP 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.2%; Score 173.5; DB 1; Lenyum 19.6%; Pred. No. 0.062; Indels 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                     337
                                                                                                                                                                                                                                                                                            199
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RP SI	RP Cape RT THE RT	RESULT 8 MYSS RAB ID MYS AC PO2 DT 01- DT 15- DT 15- DT 02- DT 05- DT 07- DT 07	B 8	B 8	Db Qy	g Q	₽ Q	g Qy	B Q	g Qy	Db
QUIENCE OF 409-1084 FROM N.A. DIINE-87304245; PubMed=3305014; DIINE-87304245; PubMed=3305014; Eda K., Sczakiel G., Wittinghofer A.; haracterization of cDNA coding for the complete light meromyos prition of a rabbit fast skeletal muscle myosin heavy chain."; r. J. Biochem. 167:97-102(1987). FUNCTION: Muscle contraction. FUNCTION: Muscle myosin is a hexameric protein that consists heavy chain subunits (MHC), 2 alkali light chain subunits (MHC), 2 alkali light chain subunits (MHC-2). and 2 regulatory light chain subunits (MHC-2). SUBCELLULAR LOCATION: Thick filaments of the myofibrils. SUBCELLULAR LOCATION: Thick filaments of the myofibrils.	NOURNCE OF 1-258. ppony JP., Elzinga M.; ppony JP., Elzinga M.; ppony JP., Elzinga M.; he amino acid sequence of rosin."; OUBNCE OF 259-428. DILINE-85131142; PhbMed=397 LR.C., Wong A.; LR.C., Wong A.; he amino acid sequence and spion in myosin subfragment spion in myosin subfragment gion in Chem. 260:3456-3461	RABIT MYSS_RABIT STANDARD; PRT; 1084 AA. P02562; 21-JUL-1986 (Rel. 01, Created) 01-JAN-1990 (Rel. 13, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Myosin heavy chain, skeletal muscle (Fragments). Oryctolagus cuniculus (Rabbit). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus. NCBI_TaxID=9986; 11	615 MYKH 618 	575 VEEREMLIKDQEKKMEDMKKRHHEEIFDLEKEFDEALEQL 614	517 ERRDAKEENFEMLQQQERAKVVGQQQQNINPSSNDDCRKRAEEVSSFIEFQEKEMEEF 574	468SLEIMSEKLRETAEDURIVRQREKMQHEQUREEMDAHDREFMDSIKQIH 516 :: : : : : : : : :: 600 KLHKAQTELELLKEKIREKSRLVKEFKELYRVERLEDYEESLKEEINYINSKLQEIE 656	434 VVKELRQISEDN QQLNYFKNKLS-KQNKHAKVLEE 467	394 SGGVRQLYGFLATKQDLDIFNQHSQGKTRLKFELKSYQEM	350 GHRGMSVLMFESSATGYLEAERLHRELAEMGLDRIAWGQKRSMF 393	296 EKDYETVWPPMYTIMNTRLDKDDNDKWIGMGNOELLEYFDKYEGLKAKHSYGPQ 349 :: :: :: :: :: :: :: :: :: :	38LEHRLKKLQEIKEIL-KELSQLSSSLKEK 3

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Query Match
Best Local S
Matches 124
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NON CONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         curricles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myosin; Muscre L
ATP-binding; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the En European Bioinformatics Institute. There are no rest; by non-profit institutions as long as its content; by descriptions as long as its content in the statement is not removed. Usage by and the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; A02985; A02985.
; A05280; A05280.
; S00084; S00084.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              split further into 2 globular subfragments (S1) and 1 rod-shaped
subfragment (S2).
SIMILARITY: Contains 1 myosin-like globular head domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils and muscles can be split into 1 light meromyosin (LMM) and 1 heavy meromyosin (HMM). It can later be
                                                                                                                                                                                                                                                                                                                                   364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       504
                                                                                                                                                                                    463
                                                                                                                                                                                                                                                           404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X05958; CAA29391.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                     AELQRAMSK-
ASERVQLLHTQN---TSLINTKKKLETDISQI----QGEMEDIVQEARNAEEKAKKAITDA
                                                                                                                                                                   TGYLEA----ERLHRELAEMGLDRIAWG---
                                                                                                                                                                                                                                                                                                                                                                                                                                              LAQRLQDAEEHVEAVNS-----KCASLEKTKQRLQNEAEDL-----MIDVERSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GARRVKLHRELAEVLEKDLOMRGASVIPCGEIYGOWKGLGEDEKDYEIVWPPMVIIMNT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARGGSAQHTAVQEFPDVEDDVDNASEEEND----SDALDDS--DDDLASDDYDSDVSQK
                                                                                                                                                RVVESMQSTLDAEIR----SRNDALRIKKKMEGDLNEMEIQLNHANRQAAEAIKNLRNTQG
                                                                                                                                                                                                                                                          LATKODLDIFNOHSOGK-TRLKFELKSYQEMVVKELRQISEDNOQLNYFKNKLSKQNKHA
                                                                                                                                                                                                                                                                                              LDHLETLKRENKNLQQEISDL-TEQIAESAKHIHELEKVKKQIDQEKSELQAALEEAEGS
                                                                                                                                                                                                                                                                                                                                                                       ATCARMDKKQRN-----FDKVLAEWKHKYEETQAELEASQKESRSLSTEVFKVKNAYEES
                                                                                                                                                                                                                                                                                                                                                                                                        ----RLDKDDNDKWLGMGNQELLEYFDKYEALRARHSYGPQGHRGMSVLMFE----SSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHGSRKONKWFKKFFGSLDSLSIEQINEPQROWHCPACONGPGAIDWYNLHPLLAHARTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nltigene :
                                                                                                               QIH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  >258
259
1084
1084
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405
408
421
423
                                QNINPSSNDDCRKRAEEVSSFIEFQEKEMEEFVEE--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -QAFTQQIEGLKRQLEEETKAKSALAHALQSSRRDCDLLREQYEEEQEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91;
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COILED CC
L -> V.
V -> L.
E -> D.
S -> G.
K -> R.
3 MW; 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----ANSEVSQWR-TKCET----DAIQRTEELEEAKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 173; DB
Pred. No. 0.07
91; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALPHA-HELICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coil; Thick filament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229CFD69A6E1F7F0
                                                                                                           ERR----DAK-EENFEMLQQQERAKVVGQQQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
.074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (S2 AND LMM DOMAINS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAILPIECE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184; Indels 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1084;
                                                                                                                                                                                                                                                                                                                                   -----OKRSMFSGGVRQLYGF
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RA Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Bagguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bardy C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Clegg S.M., Cobby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Clegg S.M., Cobby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Conroy D., Coxby N.R., Fleming K., French L., Garner A.A.,
RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Hail R.E., Hail-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA McClay J., Mclaren S., McMurray A.A., Mine S.A., Mortimore B.J.,
RA McClay J., Mclaren S., McMurray A.A., Nine S.A., Mortimore B.J.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Wijht C.L., Hubbard T., Bartley D.R., Beck S., Rogers J., Shimizu N.,
RA Wijht C.L., Hubbard T., Bartley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
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(9942D6; O944797; Q95DW1; Q95TT7; Q95TT7; Q95Y9.

28-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

TRIO and F-actin binding protein (Protein Tar. repeat on actin) (HRIHFB2122).

TRIOBP OR TARA, OR KIAA1662.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakajima D., Okazaki N., Yamakawa H., I
"Construction of expression-ready cDNA
"Curation of 330 KIAA cDNA clones.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20057165; PubMed=10591208;
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Hirosawa M., Nagase T., Murahashi Y.,
"Identification of novel transcribed
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Mammalia; Eutheria;
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Zhan M., Zhang G., Chissoe S., Murray J., Miler N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shakh T., Kurahashi H., Saitta S.,
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
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RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA A., Lane L., Tilahun Y., Wright H.;
RY "The DNA sequence of human chromosome 22.";
L. Nature 402:489-495(1999).
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Wang
Zhan
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                                                                                                                                                                                                                                                                                                                                                                                                          "Selection system for genes encoding nuclear-targeted proteins.";
Nat. Biotechnol. 16:1338-1342(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Fetal brain;
MEDLINE=99068504; PubMed=9853615;
Ueki N., Oda T., Kondo M., Yano K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 340-563 FROM N.A., AND
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                                                                                  This
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3 O 0
                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: May regulate actin cytoskeletal organization, cell spreading and cell contraction by directly binding and stabiling action. The localized formation of Factin present in stress complexes coordinates the amount of Factin present in stress complexes coordinates the amount of Factin present in stress complexes coordinates the amount of Factin present in stress complexes coordinates the amount of Factin present in stress contraction.
s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                               TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                         complexes coordinates the amount of F-actin present in fibers. May also serve as a linker protein to recruit required for F-actin formation and turnover. SUBUNIT: Binds to TRIO and F-actin. May also interact
                                                                                                                                              for genes encoding nuclear-targeted protein. SIMILARITY: Contains 1 PH domain.
                                                                                                                                                                                                       and placenta.

DOMAIN: Contains at least 2 actin-binding
                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Nuclear and
                                                                                                                 CAUTION: Ref.6 sequence differenceshift in position 478.
                                                                                                                                                                               MISCELLANEOUS: Has
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                                                                                                                                                                                    been identified in Ref.6
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                                                                                                                                       differs from that shown
                                                                                                                                                                                                                                                  expressed. Highly expressed in heart
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Matches 110
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EMBL; BC003618; AAH03618.1; -.

EMBL; BC004303; AAH034303.1; -.

EMBL; BC013278; AAH103278.1; ALT_INIT.

EMBL; BC013278; BAA3278.1; ALT_FRAME.

EMBL; AB015343; BAA34800.1; ALT_FRAME.

GO; GO:0015629; C:actin cytoskeleton; NAS.

GO; GO:0017629; F:F-actin capping activity; NAS.

GO; GO:001749; F:GTP-Rho binding; NAS.

GO; GO:0045159; F:myosin II binding; NAS.

GO; GO:0030047; P:actin modification; NAS.
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EMBL; AB051449; BAB33332.2; AI
EMBL; Z83844; CAB42898.3; -
EMBL; BC003618; AAH03618.1;
EMBL; BC004303; AAH04303.1; -
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                                                                                                                                                                                                                     EVPAGE--GPRRGLG------APLTEDQQNRLSEETEKKWQELEKLPLRENKRVPL
                                                                                                                                                                                                                                                                                           VIPCGEIYGQWKGLGEDEKDYEIVWPPMVIIMNTRLDKDDNDKW------
                                                                                                                                                                                                                                                                                                                    QALDYVELSPLTQASPQRARTPARTPDRLAKQ--EELERDLAQRSEERRKWFEATDSRTP 226
                                                                                                                                                                                                                                          LGMGNQ------ELLEYFDKYEALRAR-HSYGPQGHRGMSVLMFESSA---TG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      email to license@isb-sib.ch).
                                                                                                                                            KTRLKFELKSYQEMVVKELRQISEDNQQLNYFKNKLSKQNK-HAKVLEESLEIMSEKL-R
                      IASQGWGNGCGRSNERSSCELEVLLRVKENELQYLKKEVQCLRDELQMMQKDKRFTSGKY
                                                                                                                      ASAIEAMKKAYQEELSRELSK----TRSLQQGPDGLRKQHQSDVEALKRELQVLSEQYSQ
                                                                                                                                                                     YISQEACERSLAEMESSHQQVMEELQRHHERELQR------LQQEKEWLLAEETAAT
----KKMEDMKKRHHEEIFDLEKEFDEALEQLMYKHGLHN
                                              ERAKVVGQQQQNINPSSNDDCRKRAEEVSSFIEFQEKEMEEFVEEREMLIKDQE-----
                                                                       KCLEIGALMRQAEEREHTLRRCQQEGQELLRHN
                                                                                             RTAEDNRIVRORTKMOH-----EQNREEMDAHDRFFMDSIKQIHERRDAKEENFEMLOOO
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g; Coiled coil; Nuclear protein.
pH.
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
MT -> RR (IN REF. 2 AND 3).
EE -> GT (IN REF. 5; AAH13278).
MISSING (IN REF. 4).
MISSING (IN REF. 1).
S -> T (IN REF. 1).
S -> T (IN REF. 1).
S -> T (IN REF. 5; AAH04303).
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pred. No. 0.04;
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M -> I (IN REF. 1).
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fam; Provo.; Additional Provo.; Additional Proposition; P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: Substrate of transglutaminase. Some 200 arginines probably converted to citrullines by peptidylarginine similarity: In the N-terminal section; belongs to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 calcium-binding domains. Domains 2-4, 6, and 8 are almost entialpha-helical, configured as a series of peptide repeats of varying regularity, and are thought to form a single-stranded alpha-helical rod stabilized by ionic interactions. Domain 6 ithe most regular and may bind KIF directly by ionic interactic Domains 5 and 7 are less well organized and may induce folds ithe molecule. Domain 9 contains the C-terminus, conserved amor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELOPMENTAL STAGE: Expressed during late differentiation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: Homodimer (Probable).
TISSUE SPECIFICITY: Found in the hard keratinizing tissues such the inner root sheath (IRS) of hair follicles and medulla, and i the filiform papillae of dorsal tongue epithelium (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitted (DEC-1992) to the EMBL/GenBank/DDBJ databases. FUNCTION: Intermediate filament-associated protein that associates in regular arrays with keratin intermediate filaments (KIF) of the inner root sheath cells of the hair follicle and the granular layer of the epidermis. It later becomes cross-linked to KIF by isodippytide bonds. It may serve as scaffold protein, together with involucrin, in the organization of the cell envelope or even anchor the cell envelope to the KIF network. It may be involved in its own calcium-dependent roots-matherial servers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN: Consists of nine domains. Domain 1 contains two
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                                                                                                                                                                                                                                                                                                                                                                                                            P02633; 4ICB
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ed (DEC-1992)
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IPR002048; EF-hand.
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detazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rogers G.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAA79519.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contains 2 EF-hand calcium-binding domains
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30, Last sequence up
42, Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                S100.
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                                                                                                                                                                                                                 "Replacement of threonine residues by phosphorylatable heavy chain fragment FEBS Lett. 269:239-243(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MHCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P08799;
01-NOV-1988
MEDLINE=95345066; PubMed=7619795;
                    X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
                                                                 FEBS
                                                                                                                            Wagle G.,
                                                                                                                                                  MEDLINE=88112226; PubMed=2828113;
                                                                                                                                                                                                                                                                                   Gerisch G.;
                                                                                                                                                                                                                                                                                                                                                    STRAIN=AX2
                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION SITES,
                                                                                                                                                                                                                                                                                                                                                                                                                                 "Conserved protein domains in a myosin Dictyostelium discoideum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=87092266; PubMed=
Warrick H.M., de Lozanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
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                                                                                       Dictyostelium myosin
                                                                                                                                                                         PHOSPHORYLATION SITES
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                                                                                                                                                                                                                                                                                                                           MEDLINE=90353583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-2004
                                                                                                          Vagle G., Noegel A., Scheel J., Gerisc
Phosphorylation of threonine residues
                                                                 Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DICDI
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                                                                 227:71-75 (1988)
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                                                                                                                                                                                                                                                                                                                                                                                                                 Acad.
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(Rel. 12, Last seq
(Rel. 43, Last ann
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                                                                                                                                                                                                                                                                                                  PubMed=2387408;
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                                                                                     chain.";
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Smith C.A., Rayment I., "X-ray structure of the magnesium(II)-pyrophosphate complex of the truncated head of Dictyostelium discoideum myosin to 2.7-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95345067; PubMed=7619796; Smith C.A., Rayment I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rayment I.; "Rayment I.; "X-ray structures of the myosin motor domain of Dictyostelium "X-ray structures of the myosin motor domain of Dictyostelium discoideum complexed with MgADP.BeFx and MgADP.AlF4-."; Biochemistry 34:8960-8972(1995).
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MEDLINE=96206189; PubMed=8611530;
Smith C.A., Rayment I.;
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Bauer C.B., Kuhlman P.A., Bagshaw C.R., Rayment I.;

Bauer C.B., Kuhlman P.A., Bagshaw C.R., Rayment 
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MEDLINE=97452580; PubMed=9305951;
Gulick A.M., Bauer C.B., Thoden J.B., Rayment I.;
Gulick A.M., Bauer C.B., Thoden J.B., Rayment I.;
"X-ray structures of the MgADP, MgATPgammaS, and MgAMPPNP
"X-ray structures of the MgADP, and MgATPgammaS, and MgAMPPNP
of the Dictyostellum discoideum myosin motor domain.";
of the Dictyostellum discoideum myosin motor domain.";
Biochemistry 36:11619-11628(1997).
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                                                                                                                                                                             the European use by non-profit instruction modified and this statement modified are requires a license
                                                                                                                                                                                                                                                                                              This
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                                                                                                                                                                                                                                                                         between
                                                                                                                                                                                                                                                                                                                                  cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils. Characteristic for alpha-helical coiled coils prw. Phosphorylation inhibits thick filament formation and reduces the actin-activated APPase activity.

MISCELLANEOUS: Dictyostelium myosin II has no K(2)EDTA ATPase MISCELLANEOUS: Dictyostelium myosin II has no K(2)EDTA ATPase activity, perhaps correlated with the absence of a Cys at the SH-1 position (688).

SIMILARITY: Contains 1 myosin-like globular head domain.

SIMILARITY: Contains 1 IQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: Each myosin heavy chain can be split into 1 light meromyosin (LMM) and 1 heavy mercomyosin (HMM). It can be further split into 2 globular subfragments (S1) and 1 rod-shaped subfragment (S2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: HIGHEST CONCENTRATION IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gubfragment
DOMAIN: The
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een the Swiss Institute of Bioinformatics and the EMBL outst
Buropean Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
the statement is not removed. Usage by and for com-
fied and this statement is not removed.
                                                               1MMA;
                                                                                                     A26655;
                                             1MMG;
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03-DEC-97.
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17-AUG-96.
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                                                                                                                                                  equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The rodlike tail sequence is highly repetitive,
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ProDom; PD000355; myosin_head;
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Pfam; PF02736; Myosin
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IPR001609; myosin_head.
IPR004009; Myosin_N.
IPR008989; Myosin_S1_N.
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        MYH4_RABIT STANDARD; PRT; 1938 AA. Q28641; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-MAR-2004 (Rel. 43, Last annotation update) Myosin heavy chain, skeletal muscle, juvenile
                                                                                 RABIT
 Oryctolagus cuniculus (Rabbit).
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                                                                                                                             IKRLNEELSELRSVLEEADER 1473
                                                                                                                                                                            AERSKKKAEFDLEEAVKNLEEETAKKVKAEKAMKKAETDYRSTKSELDDAKNVSSEQYVQ
                                                                                                                                                                                                  QEK----EMEEFV----EEREMLIKDQ------EKKMEDMK------
                                                                                                                                                                                                                          KKAVTEAKNKKESELDEI KRQ-YADVVSSRDKSVEQLKTLQAKNEELRNTAEEAEGQLDR
                                                                                                                                                                                                                                                -----PSSNDDCRKRAEEVSSFIEF
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                                                                                                                                                                                                                                                                                               EKLRRTAEDNRIVRQRTKMQH-----EQNREEMDAHDRFFMDSIKQIHERRD------
                                                                                                                                                                                                                                                                                                                      QLAEETAAKQALDKLKKKLEQELSEVQTQLSEANNKNVNSDSTNKHLETSFNNLKLELEA
                                                                                                                                                                                                                                                                                                                                            Q----EMVVKELRQ-ISEDNQQLNYFKNKLSKQNKHAKVLEES----LEIMS
                                                                                                                                                                                                                                                                                                                                                                    ISELOSTIAKLEKI-----KSTLEGEVARLOGELEAEQLAKSNVEKOKKKVELDLEDKSA
                                                                                                                                                                                                                                                                                                                                                                                           LAEM-----GLDRIAWGQKRSMFSGGVRQLYGFLATKQDLDIFNQHSQGKTRLKFELKSY
                                                                                                                                                                                                                                                                                                                                                                                                                    ---NRDALE--KKKKALDAMLEEMKDQLESTG----
                                                                                                                                                                                                                                                                                                                                                                                                                                         GMGNQELLEYFDKYEALRAR-----HSYGPQGHRGMSVLMFESSATGYLEAERLHRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLEK----DLQMRGASVIPCGEIYGQWKGLGEDEKDYEIVWPPMVIIMNTRLDKDDNDKWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVEELTESFSEESKDKGVLEKTRVRLQSELDDLTVRLDSETKDKSELLRQKKKLEEE---
                                                                                                                                                   -KRHHEEIFDLEKEFDEALEQ 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 171.5; D
Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---SNVEKSKKTLE----SQLVAVNNELDEEKK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ALAAETAAKLAQEAANKKLQGEYTE
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                                                                                                                                                                                                                                                                                                                                                                                                                    -GEKKSLYDLKVKQESDMEALRNQ
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Matches 121
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                                                                                                                                                                                                                                                                             PRINTS; PR00193; MYOSINHEAVY ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinf
the European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                essential and regulatory light chains."; Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                      SEQUENCE
                                                                                                                                                                                                              Calmodulin-binding;
                                                                                                                                                                                                                                                      SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC;
                                                                                                                                                                                                                                                                                                                        Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001609; myosin_head.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Isolation, sequencing of myosin heavy chain cDNA from r
skeletal muscle and a novel cosynthesis of S-1 fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maeda K., Hostinova Wittinghofer A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=New Zealand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                             Myosin;
                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                              Pfam; PF01576; Myosin
                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                  MIAMOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and 2 regulatory light chain subunits (MLC-2).
SUBCELLULAR LOCATION: Thick filaments of the mofibrils.
DOMAIN: The rodlike tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils.
MISCELLANEOUS: Each myosin heavy chain can be split into 1 light meromyosin (LMM) and 1 heavy meromyosin (HMM). It can later be split further into 2 globular subfragments (S1) and 1 rod-shaped
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Muscle myosin is a hexameric protein that consist heavy chain subunits (MEC), 2 alkali light chain subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subfragment (S2).
SIMILARITY: Contains 1 myosin-like globular head domain.
SIMILARITY: Contains 1 IQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Muscle contraction
                                                                                                                                                                                                                                                                                                                                                                                                                                         ; U32574; AAA7419
A59293; A59293.
121;
                                                                                                                                                                                                                                                                                                                                                       PF00612; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                             P13538; 2MYS
              Similarity
                                                                                                                                                                                                                                         PS50096; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                           IPR000048; IQ_region
 Conservative
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                                                                                                                                                                                                                           protein;
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a E., Roesch-Kleinkauf A., Schu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
H
                                                                                                                                                                                              ein; Coiled coil; Thick filament; Actin-binding;
ATP-binding; Methylation; Multigene family.
783 MYOSIN HEAD-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a novel cosynthesis of atory light chains.";
              5.1%;
21.1%;
                                                       223064
                                                                                                                                                                                                                                                                                                            _N; 1.
_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         .•
                                                      MW; D8A8A2EC5B182626
Score 169; DE
Pred. No. 0.23
94; Mismatches
                                                                   METHYLATION
METHYLATION
METHYLATION
                                                                                                        ATP (POTENTIAL).

ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

METHYLATION (MONO-) (BY SIMILARITY).
                                                                                                                                                                    COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                   1
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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         There are no restrictions ong as its content is in
              DB 1;
                                                                    (TRI-)
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                                                                    (BY SIMILARITY).
(BY SIMILARITY).
(BY SIMILARITY).
                          Length 1938;
                                                         CRC64;
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to the KIF network. It may be

work. It may be involved in processing during terminal

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EF-hand

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ID TRHY HUMAN
AC Q07283;
DT 01-OCT-1994
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CC MARMALIA
RT SEQUENCE FROM NCBI TAXID=
RA SEQUENCE FROM MEDLINE=9328
RA Lee S.-C., I
RA STAILES
RA MEDLINE=9328
RA LOUENCE OF REPORTIONAL I
RT INCHING) provent of the second of the
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-93280194; PubMed=7685034;
Nee S.-C., Kim I.-G., Marekov L.N
                                                                                                                                      MEDLINE=93315897; PubMed=7686953;
O'Keefe E.J., Hamilton E.H., Lee S.-C., Steinert P.M.;
"Trichohyalin: a structural protein of hair, tongue, n
                                                                                                                                                                                                                         envelope precursor,
linking) protein.";
J. Biol. Chem. 268:1
                                                                                                                                                                                                                                                                                                               Lee S.-C., Kim
Steinert P.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trichohyalin.
THH OR TRHY OR THL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1994
15-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q07283;
01-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606
                                                                                                      epidermis."
J. Invest. I
                                                                                                                                                                       SEQUENCE OF 1731-1
MEDLINE=93315897;
                                                                                                                                                                                                                                                                               functional EF-hand-like
   FUNCTION: Intermediate filament-associated protein that associated in regular arrays with keratin intermediate filaments (KIF) of the inner root sheath cells of the hair follicle and the granular layer of the epidermis. It later becomes cross-linked to KIF by isodipeptide bonds. It may serve as scaffold protein, together with involucrin, in the organization of the cell envelope or even
                                                                                                                                                                                                                                                         structure of human trichohyalin. Portional EF-hand-like calcium-binding lope precursor, and an intermediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLKRENKNLQQEISDL-TEQIAEGGKRIHELEKVKKQVEQEKSELQAALEEAEASLEHE
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                                                                                                          Dermatol. 101:65S-71S(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                          FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence update)
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                                                                                                                                                                                            CHARACTERIZATION
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                Pfam; PF00036; efhand; 1.
Pfam; PF01023; S 100; 1.
ProDom; PD003407; CaBp S100;
PROSITE; PS00018; EF HAND;
PROSITE; PS00303; S100_CABP
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L09190; AAA65582.1;
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                                                                                                                                                                   REPEAT
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its own calcium-dependent p
differentiation.
SUBUNIT: Monomer (Probable)
TISSUE SPECIFICITY: Found i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO:0005856; C:cytoskeleton;
GO:0005509; F:calcium ion b:
erPro; IPR001751; CaBP_S10.
erPro; IPR002048; EF-hand.
erPro; IPR002017; Spectrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           calcium-binding domains. Domains 2-4, 6, and 8 are almost entirely alpha-helical, configured as a series of peptide repeats of varying regularity, and are thought to form a single-stranded alpha-helical rod stabilized by ionic interactions. Domain 6 is the most regular and may bind KIF directly by ionic interactions. Domain 5 and 7 are less well organized and may induce folds in the molecule. Domain 9 contains the C-terminus, conserved among the molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: Found in the hard keratinizing tissues such the inner root sheath (IRS) of hair follicles and medulla, and the filiform papillae of dorsal tongue epithelium (Probable). DEVELOPMENTAL STAGE: Expressed during late differentiation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ween the Swiss Institute of Bioinforma
European Bioinformatics Institute. Th
by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            different species.

TM: Substrate of transglutaminase. Some 200 arginines probably converted to citrullines by peptidylarginine (SIMILARITY: In the N-terminal section; belongs to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: Consists of nine domains. Domain 1 contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Contains 2 EF-hand calcium-binding domains.
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sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         email to license@isb-sib.ch)
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                390
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s-100 LIKE.
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EF-HAND 2 (HIGH APFINITY) (PO
6 X 13 AA TANDEM REPEATS OF
R-R-E-Q-E-E-R-R-E-Q-Q-L.
1-1 (APPROXIMATE).
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22-54
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4-1.
4-2.
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(See http://www.isb-sib.
                                                    APPROXIMATE TANDEM REPEATS. TANDEM REPEATS.
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to form a single-stranded
                                                                                                                                                                                                                                               OF R-R-E-Q-Q-L.
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             TISSUE=Extraocular muscle;
MEDINE=99318869; PubMed=10388558;
Weiss A.; Schiaffino S., Leinwand L.A.;
"Comparative sequence analysis of the coheavy chain family: implications for fur J. Mol. Biol. 290:61-75(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
DOMAIN
                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
 SEQUENCE OF 1917-1938 FROM N.A.
                                                                SEQUENCE FROM N.A.
                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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; Primates;
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Q -> K (I
V -> G (I
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                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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-> G (IN REF. 2).
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L (IN REF.
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extraocular (MyHC-eo)
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                         functional
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                                complete human sarcomeric myosin
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                        diversity.";
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GO; GO:0005859; C:muscle myosin; TAS.
GO; GO:0003779; F:actin binding; NAS.
GO; GO:0005524; F:ATP binding; NAS.
GO; GO:0005526; F:calmodulin binding; NAS.
GO; GO:0005776; F:muscle motor activity; T.
GO; GO:0006936; P:muscle contraction; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Winters L.M., Briggs M.M., Schachat F.;
"The human extraocular muscle myosin heavy chain
the cluster of fast and developmental myosin gene
Genomics 54:188-189(1998)
                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00193; MYOSTNHEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin_head.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
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EMBL; AF075248;
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                                                                                                                                                                                                                                                                                                                                                          MOD RES
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Calmodulin-binding; ATP-bindi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Extraocular muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          heavy chain subunits (MHC), 2 alkali light chain subunits (MLC) and 2 regulatory light chain subunits (MLC-2). SUBCELLULAR LOCATION: Thick filaments of the myofibrils. DOMAIN: The rodlike tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subfragment (S2).
SIMILARITY: Contains 1 myosin-like
SIMILARITY: Contains 1 IQ domain.
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MISCELLANEOUS: Each myosin heavy chain can be split into 1 light
meromyosin (LMM) and 1 heavy meromyosin (HMM). It can later be
split further into 2 globular subfragments (S1) and 1 rod-shaped
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Muscle contraction. SUBUNIT: Muscle myosin is a h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       603487;
                                                                                                                            115 SRKYD-----NNFVAPPPVSRPPLEGGWNWQARGGSAQHTAVQEFPDVEDDVDNASEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00612; IQ; 2.
PF00063; myosin_head; 1.
PF02736; Myosin_N; 1.
PF01576; Myosin_tail; 1.
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                                                                                                                                                                                                                          Similarity
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PS50096; IQ; 1.
Minable protein; Coiled coil; Thick filament;
Minable protein; Coiled coil; Thick filament;
NDSDALDDSDDDLAS--
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1938
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ACTIN-BINDING (BY SIMILARITY).
METHYLATION (TRI-) (POTENTIAL)
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30-MAY-2000 (Re
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
31-MAY-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
Hyaluronan mediated motility receptor (Intracellular hyaluronic acid
Hyaluronan mediated motility receptor for hyaluronan-mediated motility) (CD168
                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                 HMMR OR IHABP OR RHAMM.
                                                                                                                       MEDLINE=98264864; PubMed=9601098;
Assmann V., Marshall J.F., Fieber C.,
"The human hyaluronan receptor RHAMM
protein in breast cancer cells.";
J. Cell Sci. 111:1685-1694(1998).
                                                                                                                                                                                                                                                    Homo sapiens (Human).
MEDLINE=97045829; PubMed=8890751;
Wang C., Entwistle J., Hou G., Li Q., T
"The characterization of a human RHAMM hyaluronan-binding domains.";
Gene 174:399-306(1996).
-1- FUNCTION: Involved in cell motility
HMMR, the phosphorylation of a numb
                                                                                                                                                                                 TISSUE=Breast carcinoma;
                                                                                                                                                                                           SEQUENCE FROM N.A., ALTERNATIVE
                                                                                                                                                                                                                 NCBI_TaxID=9606;
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                                      SLEIMSEK-----LRRTAEDNRIVRQRTKMQHEQNREEMDAHDRFFMDSIKQIHE
                                                              SIEKEKIDEKSETEKLLEYIEEISCASDQVEKYKLDIAQLEENLKEKNDEILSLKQSLEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=075330-2; Sequence=VSP 004286; -i- TISSUE SPECIFICITY: Expressed in breas
EMBL; AF032862; AAC32548.1; -. EMBL; U29343; AAC52049.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            focal adhesion kinase occurs. May also be involved in cellular transformation and metastasis formation, and in regulating extracellular-regulated kinase (ERK) activity.
SUBCULIT: Subunit of the HARC complex.
SUBCULITIAN LOCATION: Cell surface and cytoplasmic (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALTERNATIVE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                   normal breast tissue.

DATABASE: NAME=PROW; NOTE=PROW 2;76-84(2001);
WWW="http://www.ncbi.nlm.nih.gov/prow/guide/802868666_g.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
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VDKOTTLPASARKVKSSES----KESOKNDKDLKİLEKEIRVLLQERGAQDSR-----SLDSLS1EQINEPQRQWHCPACQNGPGAIDWYNLHPLLAHARTKGARRVKLHRELAEVL-NOELLEYFDKYE-----ALRARHSYGPQGHRGMSVLMFESSATGYLEAERL-----HREL SFPKAPLKRFNDPS-----GCAPSPGAYDVKTLEVLKGPVSFQKSQRFKQQKESKQNLN AEMGLDRIAWGOKRSMFSGGVRQLYGFLATKQDLDIFNQ-----H\$QGK-------EKDLOM-RGASVIPCGEIYGOWKGLGEDEKDYEIVWPPMVIIMNTRLDKDDNDKWLGMG --TRLKFELKSYQEMVVKELRQISEDNQQLNYFKNKLSKQNKHAK------VLEE RILSLELMKLRNKKB-----TKMRGMMAKQEGMEMKLQVTQRSLEBSQGKIAQLEGKLV IQDLETELEKWEARLNAALREKTSLS-ANNATLEKQLIELTRTNELLKSKFSENGNQKNL Conservative Alternative 75 103 277 298 322 332 645 666 133 477 567 588 84031 MW; 5.0%; 19.0%;)%; Score 165; DB)%; Pred. No. 0.12; 100; Mismatches Missing (in isoform B).
/FTId=VSP 004286.

K -> KK (IN REF. 2).
S -> R (IN REF. 2).
E -> D (IN REF. 2).
K -> T (IN REF. 2).
K -> REH (IN REF. 2).
QER -> REH (IN REF. 2).
W, EA68AD6D2A626926 CRC6 N-LINKED (GLCNAC. .) (E N-LINKED (GLCNAC. .) (I N-LINKED (GLCNAC. .) (I N-LINKED (GLCNAC. .) (I N-GRACH (GLCNAC. .) (I N-GRACH (GLCNAC. .) (I N-GRACH (GLCNAC) (I N-GR splicing; Repeat; Glycoprotein; Antigen. HYALURONIC ACID-BINDING (POTENTIAL). HYALURONIC ACID-BINDING (POTENTIAL). N-LINKED (GLCNAC...) (POTENTIAL). N-LINKED (GLCNAC...) (POTENTIAL). N-LINKED (GLCNAC...) (POTENTIAL). 1; 186; Length 724; CRC64; Indels (POTENTIAL) 102; Gaps 376 326 55 268 163 104 217 420 467

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Search o Job time	DЪ	β	Db	Ş
Search completed: April 6, 2004, 19:33:55 Job time : 22 secs	394 QAERLVKQLEEEAKSRAEELKLLEEKLKGKEABLEKSSAAHTQATLLLQEKYDSMVQSL 452	559 EVSSFIEFQEKEMEEFVEEREMLIKDQEKKMEDMKKRHHEEIFDLEKEFDEALEQL 614	334 KLQQKELQIDSLLQQEKELSSSLHQKLCSFQEEMVKEKNLFEEELKQTLDELDKLQQKEE 393	•

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	8	7	6	ۍ ت	4	ω	N	H	Result No.
189.5	190	190	192	192	194.5	198	203	208	211	215.5	233.5	242	548.5	778	3313	Score
5.7	5.7	5.7	5.8	5.8	5.9	6.0	6.1	6.3	6.4	6.5	7.0	7.3	16.6	23.5	100.0	Query Match
638	639	635	2760	634	447	1036	628	1003	634	629	644	647	170	304	625	Length
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Q9LHB1	Q8W563	Q9C7B0	Q815Y2	Q9S9P3	Q8H8B2	Q9DUM3	6rst8ð	Q91LX9	Q9SAI1	Q9SBW2	Q9SMN2	Q8VZ79	Q7XYE6	Q7XY17	Q9LDX1	Į.
Q9lhb1 arabidopsis	Q8w563 triticum mo	Q9c7b0 arabidopsis	Q8i5y2 plasmodium	Q9s9p3 arabidopsis	Q8h8b2 oryza sativ	Q9dum3 kaposi's sa		Q911x9 kaposi's sa			Q9smn2 arabidopsis		Q7xye6 triticum ae	Q7xy17 triticum ae	Q9ldx1 arabidopsis	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
171.5	171.5	171.5	172	172.5	172.5	172.5	173	174	174	175.5	176	176	. 177 -	177	178	178	178.5	179	179.5	180	180.5	181	183	183.5	186	186	186.5	187
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las	Q9tv61 sus scrofa	Q922j3 mus musculu				Q8bsi0 mus musculu	cae	Q9tv63 sus scrofa	Q90y37 brachydanio	Q86iq0 dictyosteli	Q8iif6 plasmodium	7	Q9qr71 kaposi's sa	dictyos		mytilus	Q04010 onchocerca		Q28021 bos taurus	O23064 arabidopsis	O48878 sorghum bic	Q9dun0 kaposi's sa	O04614 arabidopsis	Q9ltj0 arabidopsis		w	0	Q9ax36 oryza sativ

ALIGNMENTS

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Theologis A.;

Submitted

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"Arabidopsis Open Reading Frame Submitted (FEB-2003) to the EMBL EMBL; AB025633; BAA97244.1; ---
EMBL; AF239719; AAF73960.1; ---
EMBL; BT002944; AA022757.1; ---
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                                    | OQQNINPSSNDDCRKRABEVSSF1EFQEKEMEEFVEEREMLIKDQEKKMEDMKKRHHEEI
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STRAIN=cv. PH 82-2-2;
Zhao X., Li Q., Zhang X.;
Zhao X., Li Q., Zhang X.;
Isolation and expression of a new kind of gene embryogenesis in Triticum aestivum L.";
Submitched (SEP-2002) to the EMBL/GenBank/DDBJ da EMBL; AF542974; AAD80862.1;
EMBL; AF542974; AAD80862.1;
SEQUENCE 304 AA; 35958 MW; 89980215A9584208
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Q7XYE6;
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        SEQUENCE FROM N.A.
STRAIN=cv. PH 82-2-2;
STRAIN=cv. PH 82-2-2;
Li J.R., Wang F., Li Q.Z., Zhang X.S.;
"Gene isolation and expression of a new Zn-finger.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF469493; AAP80610.1; -.
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Triticoum aestivum (Wheat).
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Q8VZ79;
01-MAR-2002
01-MAR-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SUPERIM C.J., Karlin-Neumann G., Southwick A., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W., Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Nguyen M., Karlin Neumann G., Southwick A., Tripp M., Miranda M.,
Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
Ecker J., Theologis A., Davis R.W.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AY065184; AAL38360.1; -.
EMBL; BT000136; AANL5455.1; -.
InterPro; IPR005379; XH.
InterPro; IPR005379; XS.
InterPro; IPR005381; zf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; roside eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                            Hypothetical SEQUENCE 6
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                                                                                                                                                                                                                                                                                                                                                                      PF03469; XH; 1.
PF03468; XS; 1.
PF03470; zf-XS; 1.
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YK--DLLQHASGVGNSNSDKRSAKEKASHLALVKYLQQDLADSASEAEPSSKRQKNGNPI
                                                     YNLHPLLAHARTKG
                                                                                                       LSSDDEDSDISES-----EMDEYGDKMYLNLKGGKLKVRLSPQ-AFICPYCPNKKKTSFQ
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647 AA; 74824 MW;
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Pred. No. 2.2e
31; Mismatches
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Last annotation updat
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                                                                                                                                                                                                                                        Score 242; DB 10;
Pred. No. 2.3e-06;
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36;
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Matches 110
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01-MAY-2000
01-OCT-2003
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PIR; 7
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ
EMBL; AL133315; CAB62356.1; -.
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Artiguenave F., Saurin W., Weissenbach
Mayer K.F.X., Quetier F., Salanoubat M.
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rPro; IPR005381; zf.
; PF03469; XH; 1.
; PF03468; XS; 1.
; PF03470; zf-XS; 1.
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rPro; IPR005379;
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13,
25,
                                                                                                                                                                             MW;
EMDEYGDKMYLNLKGGKLKVRLSPQ-AFICPYCPNKKKTSPQ
                                                                                    Score 233.5;
Pred. No. 7.4e
38; Mismatches
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nes 192;
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edons; core en
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                                                                                                                                 Length
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Lemcke
                                                                                                                                   644;
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Query Match
Best Local
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Q9SBW2;
01-MAY-2000
01-MAY-2000
01-OCT-2002
                                                Pfam; PF03468;
Pfam; PF03470;
SEQUENCE 629
                                                                                                                                                                                                                                                                                                                                                                                                                                   Putative transcription factor X1.

P0663E10.7.

Oryza sativa (japonica cultivar-group).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

NCBI_TaxID=39947;
                                                                                               Pfam;
                                                                                                                                                                                                                                                                                                                                    STRAIN=cv. Lemont;
Chen M., Lucas J.R., Bennetzen J.L.;
"Different rates of divergence in Sh2/Al-homologous regions
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                    Gramene; Q9SBW2;
                                                                                                                                                                                 EMBL; AF101045; AAF21887.1; EMBL; AP004317; BAB90725.1;
                                                                                                                                                                                                                                  "Oryza sativa nipponbare(GA3) clone: P0663E10.";
                                                                                                                                                                                                                                                                                  STRAIN=cv.
                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                    Sasaki T.,
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                    InterPro;
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                                                                                                                   [nterPro;
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                                                                                                PF03469;
 Similarity
                                                                                                              ; IPR005379; XH.
; IPR005380; XS.
; IPR005381; zf.
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                                                                                                                                                                                                                  (NOV-2001) to the EMBL/GenBank/DDBJ
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0 (TrEMBLrel. 13, Last st
2 (TrEMBLrel. 22, Last a:
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Matsumoto T.,
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                                              ; XH; 1.
; XS; 1.
; zf-XS; 1.
9 AA; 72715 |
6.5%;
21.1%;
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annotation update)
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 215.5; DB 1
No. 8.5e-05;
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                 DB 10;
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                                                  CRC64;
                 Length
                 629;
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 InterPro;
InterPro;
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 IPR005379;
IPR005380;
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GLGEDEKDYEIVWPPMVIIMNTRLDKDDNDKWLGMGNQELLEYFDKYEALRARHSYGPQG
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QEKMDELDAMESLNQTLVIKERKSNTEMQDARKELENGLLDL
                                      QEK--EMBEFVEEREMLIKDQEK---KMEDMKKRHHEEIFDL
                                                                                                                      FMDSIKQIHERRDAKEENFEMLQQQERAKVVGQQQQNINPSSNDDCRK-RAEEVSSFIEF
                                                                                                                                                                     E-IAAKSDYDRRIIDQEKQKNAIKSSHLKLATLEQERADENVLKLVREHKREKEAA----
                                                                                                                                                                                                                ESLEIMSEKLRR----
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                                                                                                                                                                                                                                                                                                                                               TSPGLIGDHLRKNGDLKTINDLENEGARKTDKLVANLANQIEVKNRHLQELEVTYNERTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -QPLPNRDEKFVWPWMGVLVNVPTEWKDG-RQIGRSGNHLKEQLSRFCPLKIIPLWNFRG
                                                                                -VKKILKLEQQVDAKQK-LELDIQQLKGKLEVMKHM--
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                                                                                                                                                                                                             -TAEDNRIVRORTKMOHEONREEMDAHDRF
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Q9SAII PRELIMINARY;
Q9SAII;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-JUN-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                      STRAIN=cv. Columbia;
Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S., Lee J.M., Li J. Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S., Lee J.M., Li J. Gonzalez A., Liu A., Liu K., Sakano H., Koo T., Pham P., Vaysberg Howng B., Chin C., Choi E., Chiou J., Altafi H., Brooks S., Chao Q. Conn L., Conway A., Hansen N., Johnson-Hopson C., Khan S., Kim C., Lam B., Nguyen M., Palm C., Shinn P., Tambunga G., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
"Arabidopsis thaliana chromosome 1 BAC F23A5 sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                             Submitted (DEC-1999) to (EMBL; AC011713; AAF14667 PIR; E96840; E96840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
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                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                (OCT-1999)
                                                                                                                                                     Columbia;
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Last annotation update)
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Matches 107;
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Q91LX9;
01-DEC-2001
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Pfam; PF03
Pfam; PF03
Pfam; PF03
                                                                                                                                                                      Kaposi's sarcoma-associated herpesvirus (KSHV)
Viruses; dsDNA viruses, no RNA stage; Herpesvi
Gammaherpesvirinae; Rhadinovirus.
J. Virol. 75:7882-7892(2001).
EMBL; AF360120; AAK50002.1; -.
InterPro; IPR002017; Spectrin.
InterPro; IPR002033; Tropomyosin.
PRINTS; PR00194; TROPOMYOSIN.
SEQUENCE 1003 AA; 115517 MW;
                                                                                Garber A.C., Shu M.A., Hu J., Renne R.; "Dna binding and modulation of gene expression by the latency-associated nuclear antigen of Kaposi's sarcoma-associated
                                                                                                                                                                                                               ORF73
                                                                                                                                                                                                                         01-DEC-2001
01-OCT-2003
                                                                                                                        MEDLINE=21376412; PubMed=11483733;
                                                                                                                                  SEQUENCE FROM N.A.
                                                                       erpesvirus.";
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PF03468;
PF03470;
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03469; XH; 1.

03468; XS; 1.

03470; zf-XS; 1.

634 AA; 74293 MW;
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(Tremblrel. 19, Last seq
(Tremblrel. 25, Last ann
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Pred. No. 0.00016;
7; Mismatches 195;
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  C20C43308B01A0A3
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Query Match
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Matches 91
Interpro; IPKvvv.
Interpro; IPKvvv.
Pfam; PF03469; XH; 1.
Pfam; PF03478; XS; 1.
Pfam; PF03470; zf-XS; 1.
                                                                                                                                                                                                                                                                                                                       Q8LSJ9;
01-OCT-2002
01-OCT-2002
01-MAR-2003
                                                                                                   "From the Cover: Molecular characterization of meiotic across the 140 kb multigenic al-sh2 interval of maize.' Proc. Natl. Acad. Sci. U.S.A. 99:6157-6162(2002). EMBL; AF434193; AAM22636.1; -.
                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=line LH82;
MEDLINE=21980573; PubMed=11959909;
                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                               InterPro; IPR005379; XH.
InterPro; IPR005380; XS.
InterPro; IPR005381; zf.
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Pred. No. 0.
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MEDLINE-21165304; PubMed=11264383;

MEDLINE-21165304; PubMed=11264383;

MEDLINE-21165304; PubMed=11264383;

MEDLINE-21165304; PubMed=11264383;

MEDLINE-21165304; PubMed=11264383;

MIDLINE-21165304; PubMed=11264383;

MIDLINE-21165304; PubMed=11264383;

MEDLINE-21165304; PubMed=11264383;

MEDLINE-21166304; PubMed=11264383;

MEDLINE-21
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                                                                                               Interpro; IPR002017; Spectrin.
Interpro; IPR00053; Tropomyosin.
PRINTS; PR00194; TROPOMYOSIN.
NON TER 1036 1036
SEQUENCE 1036 AA; 119328 MW;
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  Local Similarity
les 87; Conserv
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     6.0%; Score 198; DB 12; 17.9%; Pred. No. 0.0018; tive 106; Mismatches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96;
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Pred. No. 0.00047;
6; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                               2959EDD2C1C042B8 CRC64;
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                                                                                                                                                                             Query Match
Best Local S
Matches 62
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SEQUENCE FROM N.A.

Wing R.A., Yu Y., Soderlund C
Currie J., Collura K.;

"Rice Genomic Sequence.";

submitted (SEP-2002) to the El
EMBL; AC099401, AANO6846.1;

InterPro; IPR005380; XS.

pfam; PF03468; XS; 1.
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Hypothetical protein.
OJ1134F05.17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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01-MAR-2003
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                                                                                                                                                                                                                                                                                     Hypothetical protein. SEQUENCE 447 AA; 4
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                                                                                  CLAC--GRSSKDFADVHGLVMHAYNPPNVDSFIDHLGLHKALCVLMGWD
                                                                                                                               CPACQNGPGAIDWYNLHPLLAHART----KGARRVKLHRELAEVLEKDLQMRGASVIPC
                                  GEIYGQWKGLGEDEKDYB----
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                       ; Score 194.5; DB 10;
; Pred. No. 0.00098;
36; Mismatches 76;
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2003 (TrEMBLrel. 24,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
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Liu S.X., Yu
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DNQQLNYFKNKLS------KQNKHAKVLEESLEIMSEKLRKTAEDNRIVRQRTKMQH
                                                                                                                                                                                                                                                                                                               EPVPRPPVVPPQLDETEPNPHNVYVWPWMGIVVNPL--KEADDKELLLDSAYWLQTLSKF
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; IPR005380; XS.
; IPR005381; zf.
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                                                                                      ESKAYGWCARADDFESQGPIGEYLSKEGQLRTVSDISQKNVQDRNTVLEELSDMIAMTNE
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Gardner M.J., Hail N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K. Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B., "Genome sequence of the human malaria parasite Plasmodium
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-AEVLEKDLQMRGASVIPCGEIYGQ-----WKGLGEDEKDYEIVWPPMVIIMNTRLDKDD 318
                                                                                                   NSSNNKIVKRTSIKN--NTIDNYNNSTIKKIIHKEONVEDQGYIDLKTKRKLIYDALDEI 1739
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                                                                                                                                                                       NEPQRQ-WHCPACQNGPGAIDWYNLHPL--LAH----ARTKGARRVKLHREL-----
                                                                                                                                                                                                                                           KENIYENSPFHTYGRPIYEKKSKNPNNYNKIKSTTHNAILKKKRKKTLNKSISINSFTKM 1681
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19.7%; Pred. No. 0.014;
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Last annotation updat
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             RA Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M., Emcke K., Rieger M., Perez-Alonso M., Obermaier B., Ra Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B., Ra Bartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier P., Ra Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P., Ra Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P., Ra Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P., Ra Wincker P., Choisne N., Artiguenave F., Robert C., Brottier P., Ra Wincker P., Cattchico L., Weissenbach J., Saurin W., Quetier F., Ra Wincker P., Cattchico L., Weissenbach J., Saurin W., Quetier F., Ra Wincker P., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G., Ra Wiedelnann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G., Ra Wiedelnann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G., Ra Raichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J., Ra Raichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J., Ra Raichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent D., Ra Raichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent D., Ra Raichelt J., Laudie M., Berger-Llauro C., Purnelle B., Masuy D., Racker B., Vitale D., Mewes H.-W., Ra Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W., Ra Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallion L.J., Jenkins J., Ra Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallion L.J., Jenkins J., Ra Mayer K.F.X., Kaul S., Malts A., Witerback T., Fujii C.Y., Shea T.P., Ra Paie G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V., Venter J.C., Ra Pareuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C., Ra Ra Rayeraki N., Shinpo S., Takeuchi C., Wada T., Ra Natanabe A., Yamada M., Yasuda M., Tabata S., Rat Tabata S., Rat Matanabe A., Yamada M., Yasuda M., Tabata S., Rat Tabata S., Rat Matanabe A., Yamada M., Yasuda M., Tabata S., Rat Tabata S., Rat Maraiche A., Makayana S., Makazaki N., Shinpo S., Takeuchi C., Wada T., Rat M
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Q9C7B0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear Cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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MEDLINE=21016720; PubMed=11130713;
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SEQUENCE FROM N.A. MEDLINE=21898330;

PubMed=11901130

"The colinearity of the Sh2/A1

\$\frac{1}{2}\All orthologous region in rice, sorghum accompanied by genome expansion in the

EMBL;

AF434705;

AAL35831.2;

IPR005379; IPR005380;

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InterPro; InterPro; maize

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Triticeae

Genetics 160:1153-1162(2002).

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Best Local
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Pfam; PF03468; XS; 1.
Pfam; PF03470; zf-XS; 1.
Hypothetical protein.
SEQUENCE 635 AA; 73841
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Pfam; PF03
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EMBL; AC069474; AAG51004
InterPro; IPR005379; XH.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative transcription factor XI.
Triticum monococcum (Binkorn wheat) (Small spelt).
Triticum monococcum (Binkorn wheat) (Small spelt).
Triticum wonococcum (Binkorn wheat) (Small spelt).
Transcription (Binkorn wheat) (Small spelt).
Triticeae; Triticum.
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IPR005380; XS.
IPR005381; zf.
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pred. No. 0.0029;
7; Mismatches 198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF03469; XH; 1.
Pfam; PF03468; XS; 1.
Pfam; PF03470; zf:XS; 1.
SEQUENCE 639 AA; 73250 MW; 6A7FD7940030F997 CRC64;
                                                                                               450 KINELSEELQDK 461
                                                                                                                                                                                                    334 ELESKMSELNARSKELDDLAAKSSHDKSNLEQEKQKNAIKSNHLKLATAEQQR----ADE-389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    606 EFDEALEQLMYK 617
                                                                                                                                                                                                                                                          493 QHEQNREEMDAHDRFFMD-SIKQIHBRRDAKBENFEMLQQQERAKVVGQQQQNINPSSND 551
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                                                                                                                                                                                                                                                                                                                                                               434 VVKELRQIS-EDNQQLNYFKNKLSKQNKHAKVLEESLEIMSEKLRRTAEDNRIVRQRTKM 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 VEP-----QOPQQISVEPQPLPNRHEKFVWPWMGVLVNVPTEWKDG-RQVGESGNRLKGE 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279 VIPCGEIYGQWKGLGED-----EKDYEIVWPPMVIIMNTRLDKDDNDKWLGMGNQELLEY 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 QGS--KLCGWVARAEDYNFPGLIGDHLRKNADLKTIDDLENEGTRKNNKLVANLANQIEV 273
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Search completed: April 6, 2004, 19:34:52 Job time: 49 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
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2: /cgn2_6/ptodata/2/
3: /cgn2_6/ptodata/2/
4: /cgn2_6/ptodata/2/
5: /cgn2_6/ptodata/2/
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length: 2000000000
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1 MSSRAGPMSKEKN
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/cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*
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/cgn2_6/ptcdata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/backfiles1.pep:*
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         GenCore version (c) 1993 - 2004
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 4 US-09-418-710-21

2 US-08-685-576-1

2 US-09-418-710-72

1 US-08-056-200-94

2 US-08-056-200-94

2 US-08-080-644-94

2 US-08-08-322A-2

2 US-09-298-568-31

US-09-298-568-31

US-09-685-871-2

2 US-08-685-871-2

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2 US-08-685-871-1

US-09-291-4170-154

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US-09-107-532A-4632

US-09-107-532A-4632

US-09-107-332A-4632

US-09-107-332A-4632

US-09-107-332A-4632

US-09-107-332A-4632
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Sequence 21, Appli
Sequence 72, Appli
Sequence 94, Appli
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Sequence 24, Appli
Sequence 2, Appli
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Sequence 31, Appli
Sequence 14, Appli
Sequence 154, Appli
Sequence 154, Appli
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CURRENT APPLICATION NUMBER: US/09/418,710

CURRENT FILING DATE: 1999-10-15

PRIOR APPLICATION NUMBER: PCT/JP98/01783

PRIOR FILING DATE: 1998-04-17

PRIOR FILING DATE: 1998-04-17

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: UP 9/310027

PRIOR FILING DATE: 1997-04-18

PRIOR APPLICATION NUMBER: UP 9/116570

PRIOR FILING DATE: 1997-04-18

NUMBER OF SEQ ID NOS: 73

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 21

LENGTH: 1972
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; ORGANISM: Homo sapiens
US-09-418-710-21
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US-09-418-710-21
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Patent NO. 6596482
GENERAL INFORMATION:
APPLICANT: Jones, Michael H.
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 113; Conserv
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152.5
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   SESOSPAFLGTSSSTLTSSPHSGTSKRRRVTDERELRIPLEYGWORETRIRNFGGRLOGE
                                                                                                                                                                                                                                                                                                --DDYDSDVSQKSHGSRKQNKWFKKFFGSL--DSLSIEQINEPQRQWHCPACQNGPGAID
                                                                                                                                                                                                                                                                                                                                      QFRGTDSDIPSSKDSEDSNEDBEEEDBEDDEEDDESDDSQSESDSNSESDTEGSEEE
                                                                                                                                                                                                                                                                                                                                                                      QARGGSAQHTAVQEFPDVEDDVDNASEEENDSDALDDSDDDLAS--------
                                                                                                                           VAYYAPCGKKLRQYPEVIKYLSRNGIMDISRDNFSFSAKIRVGDFYEARDGPQEMQWCLL
                                                                                                                                                           GASVIPCGEIYGQW------KGLGEDEKD-----YEIVW---
                                                                                                                                                                                                                                WYNLHPLL-----AHARTKGARRVKLHRELAEVLEKD-----
                                                                                                                                                                                                                                                                 DDDDKDQDESDSDTEGEKTSMKLNKTTSSVKSPSMSLTGHSTPRNLHIAKAPGSAPAALC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FastSEQ for Windows Version 4.0
                                                        KEEDVIPRIRAMEGRRGRPPNP------DRORAREESRMRRKGRPPNVGNA
                                                                                          ----PPMVIIMNTRLDKDDNDKWLGMGNQELLEYFDKY---EALRARHSYGPQGHRGMS
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       83;
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US-08-875-435B-4
US-09-382-714-24
US-09-150-867-1
US-09-866-108A-15754
US-09-866-108A-15754
US-09-866-1390-4
US-08-466-390-4
US-08-467-781-4
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US-08-487-4
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US-08-487-398-487-4
US-08-487-398-393-36160-4
US-09-439-313-378
US-09-636-215-378
US-09-636-215-378
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Length 1972; Indels 158;

Gaps

513

239 453

633

573 303

275

679 355 Result No.

Score

Query Match

179.5 1167.5 1167.5 1167.5 1167.5 1166.1 1166.1 1164.5 1164.5 1164.5 1163.1 1163.1 1169.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 1159.5 115

Database

Maximum Minimum Total number

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Scoring table:

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Perfect score:

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US-08-685-576-1
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                      US-08-685-576-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08685576 Patent No. 5906819
                                                                                        TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                  ZIF: 20007'-5107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IEM PC COMPATIONS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-131206
FILING DATE: 26-APR-1996
                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                             NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REGERENCE/DOCKET NUMBER: 166
TELECOMMUNICATION INFORMATION:
TELEPHONE: (2021672-5300
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: JP 7:
FILING DATE: 20-NOV-1995
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 8 FILING DATE: 05-JAN-1996
                                                                                                                                   TELEFAX:
                                                  TOPOLOGY:
                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           414 NQHSQGKTRLKFELK-SYQEMVVKELRQISEDN----QQLNYFKNKLSKQNKHAKVLEES
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Nakano, Takeshi
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                                                                                                                                      (202) 672-5399
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Score 179.5;
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; ORGANISM: HOMO
US-09-418-710-72
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                                                Query Match
Best Local S
                                    Best Local Similarity
Matches 128; Conserv
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Query Match

5.4%;

ENGTH:

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47 ISKKNKNKPGNTSGKTWVSQNSNPPRAWGGQQQGRGSNVSGRGNNVSGRGNGNG-----

Conservative

5.2%; 20.1%;

Score 173.5; DB 4; Pred. No. 8.6e-05; 14; Mismatches 213;

Indels Length

203;

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Best Local Similarity Matches 116; Conserv
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                                                                                                                                                                                                                                                                                     Sequence 72, Application US/09418710 Patent No. 6596482
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ fo:
SEQ ID NO 72
                                                                                                             FILE REFERENCE: 06501-042001
CURRENT APPLICATION NUMBER: US/09/418,710
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/JP98/01783
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR APPLICATION NUMBER: JP 9/310027
                                                      PRIOR APPLICATION NUMBER: JP PRIOR FILING DATE: 1997-04-18
                                                                                                                                                                                                                              APPLICANT: Jones, Michael H. TITLE OF INVENTION: TRANSCRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   509 QHKNAEYQRKADHEADKKRNLENDVNSLKDQLEDLK--
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                                                                                               FILING DATE:
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)8; Mismatches 182;
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RESULT 4
US-08-056-200-94
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                                                        SOFTWARE: Patentin Relication DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Steinert, Peter
APPLICANT: Lee, Seung-Chul
APPLICANT: Kim, In-Gyu
                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chung, Soo-II
APPLICANT: Park, Sang-Chul
TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
TITLE OF INVENTION: Mehods of Using Same
                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                         STREET: 620 Newport CITY: Newport Beach
                        APPLICATION NUMBER: US/08/056,200 FILING DATE: 30-APR-1993
                                                                                                                                                                                                                                COUNTRY:
  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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620 Newport Center Drive, Sixteenth Floor
                                                                                                                                                                                                                                  U.S.A.
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US-08-800-644-94
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 94, Application US/08800644 Patent No. 5958752
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Best Local Similarity
                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Steinert, Peter M.

APPLICANT: Lee, Seung-Chul

APPLICANT: Kim, In-Gyu

APPLICANT: Chung, Soo-Il

APPLICANT: Chung, Soo-Il

APPLICANT: Park, Sang-Chul

TITLE OF INVENTION: Trichohyalin and Transglutaminase-3

TITLE OF INVENTION: Mehods of Using Same

NUMBER OF SEQUENCES: 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: prot
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NAME: Fedrick, Michael F.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIH054.001A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (714) 760-0404
COMPUTER READABLE FORM:
                                                                                                                                                         CORRESPONDENCE ADDRESS:
                     STATE: CA COUNTRY: U. ZIP: 92660
                                                                                     CITY: Newport Beach
                                                                                                                STREET:
                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1530 RQERDRKFRLEEQKVRRQEQ----ERKFMEDEQQLRRQEGQQQLRQED 1573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1299 EEQLLQEREEQPLLRQERDRKFREEELLHQEQGRKFLEEEQRLREERERKFLKEEQQLRL 1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1239 QERRRWQQANRHFPEEEQLEREEQKEAKRRDRKSQEEKQLLREEREEKRRRQETDRKFRE 1298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       436 KELROISED------NQOLN-----YFKNKLSKONKHAKVLEESLEIMSEKLRR 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 IVWPPMVIIMNTRLDKDDNDKWLGMGNQELLEYFDKYEALR-----ARHSYGPQGHRG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IKDQEKK--MEDMKKRHHEBIFDLEKEFDEALEQLMYKHG---LHNED 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F----EMLQQQERAKVVGQQQQNINPSSNDDCRKRAEEVSSFIEFQEKEMEEFVEEREML 581
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                                                                                                                E: Knobbe, Martens, 620 Newport Center
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                                           U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -RDNKVYCKGRENEQFRQLEDSQVRDRQSQQDLQHLLGEQQERDRE 1238
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                                                                                                                , Olson
Drive,
                                                                                                                & Bear
Sixteenth
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                                                                                                                  Floor
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CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/056,200

FILING DATE: 30-APR-1993

ATTORNEY/AGENT INFORMATION:
NAME: Fedrick, Michael F.
REGISTRATION NUMBER: 36,799

REGISTRATION NUMBER: NIH054.00

TELECOMMUNICATION: TOPORMATION:
TOLECOMMUNICATION: 760-0404
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US-08-728-323A-2
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Best Local Similarity
                                                                                                 Sequence 2, Application patent No. 5948676
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US.
FILING DATE: 14-FEB-199
                    APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
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COMPUTER: II
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                                                                                                                                                                                                                                                                                                                                                      F----EMLQQQERAKVVGQQQQNINPSSNDDCRKRAEEVSSFIEFQEKEMEEFVEEREML 581
                                                                                                                                        Application US/08728323A
                                                                                                                                                                                                                                                                                                                   FLEEEQQLHRQQRQRKFLQEEQQLRRQERGQ-QRRQDRDRKFRE--EEQLRQEREEQQLS 1529
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Chang, Yuan
Bohenzky, Roy A.
Russo, James J.
Edelman, Isidore S.
Moore, Patrick S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.1%; Score 167.5; DB 2; Length 1898; 20.9%; Pred. No. 0.00024; tive 85; Mismatches 162; Indels 123;
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TOPOLOGY: linear; MOLECULE TYPE: protein US-08-728-323A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
             APPLICANT: Kieff, Elliott D.
APPLICANT: Kieff, Elliott D.
APPLICANT: Ballestas, Mary E.
APPLICANT: Kaye, Kenneth M.
APPLICANT: Kaye, Kenneth M.
TITLE OF INVENTION: WIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
TITLE OF INVENTION: WIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
FILE REFERENCE: 16412-10001R
CURRENT APPLICATION NUMBER: US/09/298,568
CURRENT FILING DATE: 1999-04-21
EARLIER FILING DATE: 1998-11-19
EARLIER FILING DATE: 1998-11-19
NUMBER OF SEQ ID NOS: 3
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SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
TREIFFERENCE - 27-778-040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1162 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: Z12-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     527 EMLQQQERAKVVGQQQQNINPSSNDDCRKRAEEV----SSFIEFQEKEMEEFVEEREMLI
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Pred. No. 0.00016;
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                                                                                                                 RESULT 9
US-09-595-684B-31
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US-09-410-399-2
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SEQ ID NO 2
LENGTH: 1162
TYPE: PRT
Sequence 31, Application US/09595684B Patent No. 6544766 GENERAL INFORMATION:
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APPLICANT: Robertson, Erle S.
APPLICANT: Cotter, Murray A.
TITLE OF INVENTION: Methods to Inhibit or Enhance the
TITLE OF INVENTION: to Genomic Host DNA
FILE REFERENCE: UM-03778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2
LENGTH: 1162
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Best Local Similarity 19.6%;
Matches 46; Conservative 6
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CURRENT FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 6
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TITLE OF INVENTION: Human kinesins and methods of
TITLE OF INVENTION: and purifying human kinesins
FILE REFERENCE: Cytop036
CURRENT APPLICATION NUMBER: US/09/595,684B
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 09/295,612
PRIOR APPLICATION NUMBER: 09/295,612
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                               853
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                                                                                                             520 DAKEENFEMLQQQE-----RAKVVGQQQQNINPSSNDDCKKRAEEVSSFIEFQEKEMEEF 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       690 LQSAFNEITKLTSLIDGKVPKDLLCNLELEGKITDL-----QKELNKEVEENEALRE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 HARTKGA----RRVKLHRELAEV-----LEKDLQMRGASVIPCGEIYGQWKGLGEDEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                468 ESDVFSNTLDTLSEIEWN-PATKLLNQENIESELNSLRADYDNLVLDYEQLRTEKEEMEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 QNKWFKKFFGSLD------SLSIEQINEPQRQWHCPACQNGPGAIDWYNLHPLLA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 ASEEENDSDALD------DSDDDLA-----SDDYDSDVSQKSHGSRK 199
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                                                                                                                                                                                                                                                                      SLEIMSEKLRRTAEDNRIVRQ-----RTKMQHEQNREEMDAHDRFFMDSIKQIHERR
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                                        NA----LESLKHQETINTLKSKISEEVSRNLHMEENTGETKD--
                                                                                                                                                                                                                                                                                                                                               EAQKFDSSLGALKTELSYKTQELQE----KTREVQERLNEMEQLKEQLENRDSPLQTVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLLEEIGKTKDDLATTQSNYKSTDQEFQNFKTLHMDFEQKYKMVLEENERMNQEIVNLSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----EVILLSELKSLPSEVERLRKEIQDKSEELHIITSEKDKLFSEVVHKESRVQ 792
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VAisberg, Eugeni
Wood, Kenneth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cara
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US-08-685-871-2
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GENERAL INFORMATION:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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APPLICANT: IWAMATSU,
TITLE OF INVENTION: R
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16887/845
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 25-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7.
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1354 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/685,871 FILING DATE: 24-JUL-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3000 K St
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 350 G-HRGMSVLMFESSATGYLEAERLHRELAEMGLDRIAWGQKR-SMFSGGVRQLYGFLATK 407
                                     657 DMLNHSEKE-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                          AILEAERRDRGHDSEMIGDLQARITSLQEEVKH-LKHNLE-----KVEGERKEAQ 656
                                                                                                                                          PLL-AHARTKG-----ARRVKLHRELAEVLEKDLQMRGASVIPCGEIYGQWKG-- 291
                                                                                                                                                                               DLLRTESDTAVRLRKSHTEMSKSISQLESLN-RELQERNRILENSKSQTDK---DYYQLQ 607
                                                                                                                                                                                                                                                                                  QHTAVQEFPDVEDDVDNASEEENDSDALDDSDDDLASDDYDSDVSQKSHGS------
                                                                                                                                                                                                                                                  OHRINEYORKAEQENEKRRNVENEVSTIKDOLEDIKKVSONSQLANEKLSOLOKOLEEAN 551
                                                                      --LGEDEKDYEIVMPPMVIIMNTRĻDKDDNDKWLGMGNQELLEYEDKYEALRARHSYGPQ 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMAMATSU, Akihiro
VENTION: RHO TARGET PROTEIN KINASE
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                              Linear
                                                                                                                                                                                                               ----RKQNKWFKKFFGSLDSLSIEQINEPQRQWHCPACQNGPGAIDWYNLH 244
                                                                                                                                                                                                                                                                                                                       5.0%; Score 164; DB 3; Length 1354;
21.3%; Pred. No. 0.00029;
ative 89; Mismatches 201; Indels 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68
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                                         -----KNNLEIDLNYKLKSL-QORLEQEVNEHKVTKARLTDKHQ 703
                                                                                                                                                                                                                                                                                                                                    Gaps
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US-08-685-576-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL
                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1388 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ito, Masaaki
APPLICANT: Takahashi, No. 5906819uaki
APPLICANT: Takahashi, RHO TARGET PROTEIN RHO-KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                           NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16887/843
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                               FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION UNMEER: JP 8-131206
FILING DATE: 26-APR-1996
FILING DATE: 16-APR-1996
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: JP 7-
APPLICATION UNMBER: JP 7-
FILING DATE: 20-NOV-1995
                                                                                                                                                                                                                                                                                                        FILING DATE: 20-NOV-PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 24-JUL-1996
                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        408 QDĻDIFNQHSOG-ĶTRLKFELKSYQEMVVKELRQISEDNQQLNYFKŅKĻSKQNKHAKVĻE 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              536 KVVGQQQQNINPSSNDDCRKRAEEVSSFIEFQEKEMEEFVEEREMLIKDQEKKMEDMKKR 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  862 ELKEETEEKNRENLKKIQELQNEKETLATQLDLAETKAESEQLARGLLEEQYFELTQESK 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                514 QIHERRDAK-EENFEMLQQ------
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Nakano, Takeshi
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APPLICANT: MARTINEZ, RICARDO
APPLICANT: WHYTE, DAVID
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0328
CURRENT APPLICATION NUMBER: US/09/688,188B
CURRENT FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 09/291,417
PRIOR APPLICATION NUMBER: 09/291,417
PRIOR APPLICATION NUMBER: 60/081,784
PRIOR APPLICATION NUMBER: 60/081,784
PRIOR FILING DATE: 1998-04-14
PRIOR FILING DATE: 1998-04-14
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US-09-688-188B-154
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US-08-685-576-4
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                                                                                                                                                                                                                                                                             Sequence 154, Application US/09688188B Patent No. 6656716
GENERAL INFORMATION:
                                                    NUMBER OF SEQ ID NOS: 155
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 154
LENGTH: 966
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Best Local Similarity
               ·09-688-188B-154
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                          ORGANISM: Murine sp
                                           TYPE: PRT
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SOFTWARE: PatentIn Ver. 2.1
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US-09-291-417D-154
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Best Local S
Matches 138
                                                                                                                                                                                  Sequence 154, Application US/09291417D Patent No. 6680170
GENERAL INFORMATION:
APPLICANT: PLOWMAN, GREGORY
FILE REFERENCE: 038602/0329
CURRENT APPLICATION NUMBER: US/09/291,417D
CURRENT FILING DATE: 1999-04-13
PRIOR APPLICATION NUMBER: 60/081,784
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 155
                                                                                                                      APPLICANT: MARTINEZ, RICARDO
APPLICANT: WHYTE, DAVID
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
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18.3%; Pred. No. 0.00026;
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; TYPE: PRT
; ORGANISM: Murine sp.
US-09-291-417D-154
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Sequence 11, Application US/09914259
Patent No. 6495336
GENERAL INFORMATION:
APPLICANT: Makowski, Lee
APPLICANT: Myman, Paul
APPLICANT: Hyman, Paul
APPLICANT: Williams, Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF
FILE REFERENCE: 8471-010-999
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US-09-914-259-11
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Best Local Similarity
Matches 138; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QDSANVTQPSLDSNK--LLQDSSTPLPPSQPQE----PVNGPCSQPSGDG-----PLQTT 390
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18.3%; Pred. No. 0.00026;
ative 121; Mismatches 238; Indels 2
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                          OF NANOSTRUCTURES
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COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

STATE: CITY: Denver

8

ADDRESSEE: Sheridan Ross P. STREET: 1700 Lincoln St., S

P.C. Suite

3500

FOR

HEART FAILURE

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; TYPE: PRT
; ORGANISM: HOMO
US-09-914-259-11
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Sequence 3, Application US/08938105
Patent No. 6353151
GENERAL INFORMATION:
APPLICANT: Leinwand, Leslie A.
APPLICANT: Viketrom, Karen L.
TITLE OF INVENTION: TRANSGENIC MODEL FO
NUMBER OF SEQUENCES:
ANDRESSEONDENCE ADDRESS:
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CURRENT FILING DATE: 2000-11-21
NUMBER OF SEQ ID NOS: 180
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 3878
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                                                                                                                               RESULT 15
US-08-938-105-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEEHTRVTDESIPSYSGSDMPRNDI-NMWSKVTEEGTELSQRLVRSGFA---GTEIDPEN 1818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HRELAEVLEKDLOMRGASVIPCGEIYGOWKGLGED--EKDYEIVWPPMVIIMNTRLDKDD 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----FGSLDSLSIEQINEPQRQWHCPACQNGPGAIDWYNLHPLLAHARTKGARRVK--L 260
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEKT.RTAEDURI------VRQRTKMQHEQUREEMDAHD-----
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                                                                                                                                                                                               VEAKPELSLEVQLQAERDAIDRKEKEITNLEEQLEQFREELENKN
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1886 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPB: protein
US-08-938-105-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CTOOK, Wannell M.
REGISTRATION UMBER: 31,071
REFERENCE/DOCKET NUMBER: 3595-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (303) 863-0223 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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1719 KKEQDTSAHLERMKKNMEQTIKDLQHRLDEA-EQIALKGG 1757
                                                                                                       1659 SERVQLLHSQNTSLINQKKKMDADLSQLQTEVEEAVQECRNAEEKAKKAITDAAMMAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                         1494 EEAEASLEHEEGKILRAQLEFNQIKAEIERKLAEKDEEMEQ-----AKRN-HLRVVD 1544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1438 EESLEHLETFKRENKNIQEEISDI-TEQIGEGGKNVHELEKIRKQLEVEKLEIQSAL--- 1493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1402 --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1358 -- AKCSSLEKTK-HRLQNEIEDLMVDVERSNAAA------AALDKKQRNFDKI--- 1401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1306 LQRVLSKANSEVAQWRTKY--ETDAIQRTEELEEAKKKL-AQRLQDAEEAVEAVN----- 1357
                                                                                                                                                                                                                  1599 LKDTQLQLDDAVRANDDLKENIAIVERRNTLLQAELEELRAVVEQTERSRKLAEQELIET 1658
                                                                                                                                                                                                                                                                                                                               1545 SLQTSLD-----AETRSRNEALRVKKKMEGDLNEMEIQLSQANRIASEAQKHLKNAQAH 1598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1248 WQLTRGKLSYT--QQMEDLKRQLEEEGKAKNALAHALQSARHDCDLLREQYEEEMEAKAE 1305
                                                                                                                                                                                                                                                                                                                                                            465 -LEESLEIMSEKLRRTÄEDNRIVRQRTKMQHEQNREEM-------DAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   408
                                                582 IKDQEKK--MEDMKKRHHEBIFDLEKBFDEALEQLMYKHG 619
                                                                                                                                                              543 --- QNINPSSNDDCRKRAEEVSSFIEFQEKEMEEFVEE--------REML 581
                                                                                                                                                                                                                                                                        505 DRFFM------DSIKQ---IHERRDA-----KEENFEMLQQQERAKVVGQQQ---- 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360 ----ESSATGYLEAERLHRELAEMGLDRIAWGQK-----RSMFSGGVRQLYGFLATK 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306 MVIIMNTRLDKDDNDKWLGMGNQELLEYFDKYEALRARHSYGPQGHRGMSVLMF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 AHARTKGARRVKLHRELAEV--LEKDLQMRGASVIPCGEIYGQWKGLGEDEKDYEIVWPP 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 GSRKQNK------WFKKFFGSLDSLS-IEQINEPQRQWHCPACQNGPGAIDWYNLHPLL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 WQARGGSAQHTAVQEFPDVEDDVDNASEEEND-SDALDDS--DDDLASDDYDSDVSQKSH 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QDLDIFNQHSQGK-TRLKFELKSYQEMVVKELRQISEDNQQLNYFKNKLSKQNKHAKV-- 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----LAEWKOKYEESOSELESSOKEARSLSTELFKLKNAY 1437
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Search completed: April 6, Job time : 26 secs

2004, 19:36:00

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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Published Applications AA:*

1: /cgn2=6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2-6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

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3313
1 MSSRAGPMSKEKNVQGGYRP.....EFDEALEQLMYKHGLHNEDD 625
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1428.5 745.5 745.2 297 298 199.5 199.5 199.5 199.5 179.5 173.5 172.5	Score
200 200 200 200 200 200 200 200 200 200	Query Match Length
611 223 188 219 227 414 448 1972 11972 11979 1969 1969 1969	
12 12 12 12 13 14 14 14	DB
US-10-425-114-58390 US-10-424-599-234018 US-10-424-599-234019 US-10-424-599-242612 US-10-424-599-178379 US-10-425-114-63998 US-10-425-114-63998 US-10-425-114-53998 US-10-425-114-53998 US-10-425-114-53998 US-10-425-114-54044 US-09-839-479-21 US-10-98-39-479-21 US-10-296-115-1265 US-10-363-616-295 US-10-363-616-295 US-10-369-493-43 US-10-369-493-43 US-10-369-493-43	ID
Sequence 58390, A Sequence 234018, Sequence 234012, Sequence 242612, Sequence 68998, A Sequence 63998, A Sequence 54044, A Sequence 21, Appl Sequence 43, Appl Sequence 1265, Ap Sequence 295, App Sequence 295, App Sequence 43, Appl Sequence 43, Appl Sequence 1265, Ap Sequence 1265, Ap Sequence 1265, App Sequence 43, Appl Sequence 43, Appl	Description

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160.5	161	161	161	161.5	161.5	161.5	161.5	161.5	161.5	162	162.5	162.5	163	163.5	163.5	164	165	166	166	166	167.5	167.5	168	170.5	170.5	170.5	170.5	170.5	T/0.5
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621	1837	725	650	3925	3911	3907	3878	1875	621	1992	709	709	287	498	308	1790	724	1162	1162	345	3917	3899	1043	725	725	725	725	725	0/0
14	15	10	15	14	15	14	14	15	15	15	15	14	14	15	12	15	15	14	12	14	14	14	15	15	15	15	14	12	4
US-10-316-253-44	US-10-369-493-22734	US-09-978-309A-47	US-10-104-047-3636	- 1	US-10-370-685-100	US-10-171-311-2	US-10-080-608A-11	US-10-369-493-22285	US-10-108-260A-4409	US-10-369-493-6527	US-10-023-634-14	US-10-256-250-15	US-10-029-386-33041	US-10-104-047-3191	US-10-425-114-64137	US-10-369-493-1586	US-10-023-634-80	US-10-294-804-2	US-09-894-273-2	US-10-029-386-34255	US-10-171-311-8	US-10-171-311-4	US-10-310-154-449	US-10-205-647A-4	US-10-023-634-79	US-10-023-634-78	US-10-256-250-14	US-10-257-377-1	02-10-020-020-10
Sequence	Sequence	Sequence					Sequence		Sequence		Sequence				Sequence	Sequence		Sequence	Sequence	Sequence					Sequence	Sequence	Sequence	Sequence	octuence
44, Appl	22734, I	47, Appl	3636, Ap	6, Appli	100, App	2, Appli	11, Appl	22285, 1	4409, Ap	6527, A	14, App	15, Appl	33041, /	3191, Ap	64137, A	1586, Ap	80, Appl	2, Appli	2, Appli	34255, I	8, Appli	4, Appli	449, App	4, Appli	79, Appl			1, Appli	דסי ישקע

ALIGNMENTS

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127 -PVSRPPLEGGWNWQARGGSAQHTAVQEFPDVED-DVDNASEEENDSDALDDS 177	71 WGGSGSSHPSGTSWAQAPDHGAATRGNPRPPSQTS 105	74 WGGQQQGRGSNVSGRGNNVSGRGNGNGRGIQANISGRGRALSRKYDNNFVAPP 126	13 RSARSMSGSGDRRGGGPPGSHSGWETMGKKSK-KPGQAGGRQWAPWSSTNVTPNTARP-A 70	33 RLASSQDDGGEWEVISKKNKNKPGNTSGKTWVSQNSNPPRA 73	cal Similarity 47.2%; 294; Conservative 99		; OTHER INFORMATION: Clone ID: LIB3079-030-A8_FLI.pep US-10-425-114-58390	ORGANISM: Zea mays FEATURE:	TYPE: PRT	SEQ ID NO 58390	NUMBER OF SEQ ID NOS: 73128	ă	FILE REFERENCE: 38-21(53313)B		APPLICANT: Cao, Yongwei TITTE OF TATEMETON: Michaic Acid Molegyles and Other Molegyles Associated With		••	••		ADDITION: [in .]inadona	PUDITATION NO. USZUU4UU3488AI	nce 58390, Application US/10425114	US-10-425-114-58390	

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APPLICANT: LA ROSA Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
ITITLE OF INVENTION: Soy Nucleic Acid Molecul
ITITLE OF INVENTION: Plants and Uses Thereof
FILE REFERENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
INUMBER OF SEQ ID NOS: 285684
SEQ ID NO 234018
LENGTH: 324
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US-10-424-599-234018
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                                                                                                                                                                                             Matches 162;
                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                       165
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                                                       61
                                                  SEEENDSDALDDSDDDLASDDYDSDVSQKSHGSRKQNKWFKKFFGSLDSLSIEQINEPQR
                                                                                                                                           GRGRALSRKYDNNFVAPPPVSRPPLEGGWNWQARGGSAQHTAVQEF--PDVEDD--VDNA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDDLASDDYDSDVSQKSHGSRKQNKWFKKFFGSLDSLSIEQINEPQRQWHCPACQNGPGA
QWHCPACQNGPGAIDWY-NLHPLLAHARTKGARRVKLHRELAEVLEKDLQMRGASVIPCG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LMFESSATGYLEAERLHRELAEMGLDRIAWGQKRSMF-SGGVRQLYGFLATKQDLDIFNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDDI-SDDYDSDASEKSFETRKTNKWFKEFFEVLNTLSLEQINEQTRQWHCPACKNGPGA
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                                                                                                                         GRPQLGTSGYESNYVTPNPVIRPPLEHGWNWQSRPGAIQSNVRDEISPEDLQKNYGVDDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIFESSAVGYMEAERLHKHFVNQGTDRNSWHLRKVRFVPGGKRQLYGFLANKEDMEAFNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDWYKGLQPLVSHARTKGSTRVKLHRELAALLEEELSRRGTSVLPAGEQFGKWKGL-QES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KA---RRFDVDSGTMKDRQLRKEYVQKFIDCQVKDVAEFEVERDELIKVHEDKKLKLKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVVGQQQQNINPSSNDDCRKRABEVSSFIEFQEKEMEEFVEEREMLIKDQEKKMEDMKKR
                                                                                                                                                                                             Conservative
                                                                                                                                                                                          22.5%; Score 745.5; DB 1
31.1%; Pred. No. 4.3e-48;
tive 68; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Molecules and Other Molecules Associated Thereof for Plant Improvement
                                                                                                                                                                                                                          DB 12;
                                                                                                                                                                                           84; Indels 207;
                                                                                                                                                                                                                            Length
                                                                                                                                                                                          Gaps
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APPLICANT: Cao Yongwei

FITLE OF INVENTION: Soy Nucleic Acid Molecu
FITLE OF INVENTION: Plants and Uses Thereo.
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 234019
LENGTH: 223
TYPE: Dom
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US-10-424-599-234019
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Best Local Simil
Matches 131; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 234019, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(223)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Clone ID: PAT_MRT3847_53343C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Glycine
                                                                                                                                                                                                                                                                                                Local Similarity
   180
                                   284
                                                                     120
                                                                                                       225
                                                                                                                                                         165 SEEENDSDALDDSDDDLASDDYDSDVSQKSHGSRKQNKWFKKFFGSLDSLSIEQINEPQR 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       584
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                                                                                                                                         13
                   | EIYGQWKGLGEDEKDYBIVWPPMVIIMNTRLDKDDNDK
                                                                                                QWHCPACQNGPGAIDWY-NLHPLLAHARTKGARRVKLHRELAEVLEKDLQMRGASVIPCG
                                                                                                                                         GEEE-ESDDLEDTDDDLMSDDDDSDASQKSHETRKKSKWYKKFFEILDGLTVEQINEPER
                                                                                                                                                                                                            GRPQLGTSGYESNYVTPNPVIRPPLEHGWNWQSRPGAIQSNVRDEISPEDLQKNYGVDDD
                                                                                                                                                                                                                                            GRGRALSRKYDNNFVAPPPVSRPPLEGGWNWQARGGSAQHTAVQEF--PDVEDD--VDNA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DQEKKMEDMKKRHHEEIFDLEKEFDEALEQLMYKHGLHNED 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLEESLEIMSEKLRRTAEDNRIVRQRTKMQHEQNREEMDAHDRFFMDSIKQIHERRDAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSYGPQGHRGMSVLMFESSATGYLEAERLHRELAEMGLDRIAWGQKRSMFSGGVRQLYGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QWHCPACQGGPGAIDWYRGLQPLVTHAKTKGSKRVKIHRELAILLDEELRRRGSAVIPPA 179
                                                                     QWHCPACQGGPGAIDWYRGLQPLVTHAKTKGSKRVKIHRELAILLDEELRKRGTSVIPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AHKDNVDAMTRRHWEEKVQLEERFNEELAKLMEKYSLSHPE 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENFEMLOQQERAKVVGQQQQNINPSSNDDCRKRAEEVSSFIEFQEKEMEEFVEEREMLIK 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EIYGQWKGLGEDEKDYEIVWPPMVIIMNTRLDKDDNDKWLGMGNQELLEYFDKYEALRAR
   EVFGKWKGLKEEEXDHEIVWPPMVVIQNTKLEQDENDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEFERMQQEKREKV----KPSSTSPLNEEEGRVKVDEYLKFVEFQDKEMENFVASEEKLRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LATKQDLDIFNQHSQGKTRLKFELKSYQEMVVKELRQISEDNQQLNYFKNKLSKQNKHAK 463
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      max
                                                                                                                                                                                                                                                                                              21.8%;
                                                                                                                                                                                                                                                                            ; Score 721; DB 12;
; Pred. No. 1.9e-46;
41; Mismatches 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecules and Other Molecules
Thereof for Plant Improvement
                                                                                                                                                                                                                                                                                40;
   217
                                   321
                                                                                                                                                                                                                                                                                                                Length 223;
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US-10-424-599-178379
; Sequence 178379, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_132093C.1.pep US-10-424-599-178379
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US-10-424-599-242612
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APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 242612
LENGTH: 188
TYPE: PRT
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                Query Match
Best Local Similarity
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                                                                                                      ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Clone ID: PAT_MRT3847_61108C.1.pep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       487 RQRTKMQHEQNREEMDAHDRFFMDSIKQIHERRDAKEENFEMLQQQERAKVVGQQQQNIN 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             427 LKSYQEMVVKELRQISEDNQQLNYFKNKLSKQNKHAKVLEESLEIMSEKLRRTAEDNRIV 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSSNDDCRK--RAEEVSSFIEFQEKEMEEFVEEREMLIKDQEKKMEDMKKRHHEEIFDLE 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------DQQDKEMDALEKNFQSQIQDIQQAIAAKEDKFVKLQLQ------AMQEKVK 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KELENELTQLMDKYNCNQSQE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEFDEALEQLMYKHGLHNEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MRSYQEMVERKIKHINDDSRKLDYYKSMVAKEQIKSQVGADSLCKSSEKLSMTTEKNRV-
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Kovalic David K
 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.0%;
7.8%; Score 258; DB 12;
33.6%; Pred. No. 1.8e-11;
tive 24; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 297; DB 12; Length 188; Pred. No. 1.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              625
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                                DB 12; Length 219;
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 Indels
 40;
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Gaps
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; OTHER INFORMATION:
US-10-425-114-68998
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US-10-425-114-68998
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                                                                                                                  Sequence 63998, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:
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Publication No. US20040034888A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 68998
LENGTH: 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Zhou, Yihua APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5331)B
CURRENT FILING DATE: 2003-04-28
UNMBER: OF SEQ ID NOS: 73128
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Zea mays subsp. mexicana
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                                                                                                                                                                                                                                                                                    169
                                                                                                                                                                                                                                                                                                                                389 KRSMFSG---
                                                                                                                                                                                                                                                                                                                                                                                109
                                                                                                                                                                                                                                                                                                                                                                                                                          337 ----YEALRARHSYGPQGHRGMSVLMFESSATGYLEAERLHRELAEMGLDRIAWGQ--- 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 GRALSRKYDNNFVAPPPVSRPPLEGGWNWQARGGSAQHTAV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    278 SVIPCGEIYGQWKGLGEDEKDYEIVWPPMVIIMNTRLDKDDNDKWLGMGNQELLEYFDK- 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 CPACQNGPGAIDWYNLHPLLAHARTKG----ARRVKLHRELAEVLEKDL-----QMRGA 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSLP----SDLVQASREDLIVWPPTVIIHNTSTGRKKDGRLEGLGNKEM----DKK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLAC--GRSSKDFADVHGLVMHAYNPPNADSLVDHLGLHKALCVLMGWDYTKVPENFKGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VDNASEEENDSDALDDSDDDLASDDYDSDVSQKSHGSRKQ 200
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                                                                                                                                                                                                                                                                                    SRSVDSDQNPLLVETDTRTAEKKRILYGYLAIASDLDELDSDSRKRASLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKGKNVLESL-PKIEQLTQGVADVNIESGQDD-GEWVVYAKKSKNRARSTTVKPWSPPVH
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SEQ ID NO 63998
LENGTH: 414
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US-10-425-114-54044
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                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Clone ID: LIB3245-195-E3_FLI.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Zea mays
                                                           NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 54044
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                                                                                                        APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(3333)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
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                                                                                                                                                                                                                                                                                                           APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua
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ORGANISM: Zea mays
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Local Similarity 20.5%;
hes 97; Conservative 9
                                          ENGTH: 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HRELAEMGLDRIAWGQKRSMFSGGVRQLYGFLATKQDLD----IFNQHSQGKTRLKFELKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESHFAAGGFGKKDWIGKKNOGS----ELYGWLARAEDYNSPGIIADH-----LRKNGDLKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSND-DCR-KRAEEVSSFIEFQEKEMEEFVEEREMLIKDQEKKMEDMKKRHHEE 599
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                                                                                                                                                                                                                        Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
Cao, Yongwei
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PRIOR APPLICATION NUMBER: US 09/418,710
PRIOR PILING DATE: 1999-10-15
PRIOR PILING DATE: 1999-04-17
PRIOR PILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: DP 9/310027
PRIOR PILING DATE: 1997-10-24
PRIOR PILING DATE: 1997-04-18
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; OTHER INFORMATION: Clone ID: UC-ZMFLMO17282F05_FLI.pep
US-10-425-114-54044
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US-09-839-479-21
US-09-839-479-21
Sequence 21, Application US/09839479
Publication No. US20020039779A1
GENERAL INFORMATION:
GENERAL INFORMATION: TRANSCRIPTIONAL
TITLE OF INVENTION: TRANSCRIPTIONAL
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CURRENT FILING DATE: 2001-04-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1972
TYPE: PRT
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ORGANISM: Homo sapiens
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nes 62; Conserv
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les 113; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 CPACQNGPGAIDWYNLHPLLAHARTKG-----ARRVKLHRELAEVLEKDL-----QMRGA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282 QSLP-----SDLVQASREDLÍVWPPTVÍÍHNTSTGRKKDGRLEGLGNKÉM----DKK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        278 SVIPCGEIYGQWKGLGEDEKDYEIYWPPWYIINNTRLDKDDNDKWLGMGNQELLEYFDK- 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           389 KRSMFSG------GVRQLYGFLATKQDLDIFNQHSQGKTRLK 424
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                                                                                                                                                                                                                                                                                                                                                                                                        140 QARGGSAQHTAVQEFPDVEDDVDNASEEENDSDALDDSDDDLAS-------
                                                                                                                                                                                  514 SESOSPAFLGTSSSTLTSSPHSGTSKRRRVTDERELRIPLEYGWQRETRIRNPGGRLQGE
                                                                                                                                                                                                                               240 WYNLHPLL-----AHARTKGARRVKLHRELAEVLEKD---
                                                                                                                                                                                                                                                                                                                184 --ppypspysokshgsrkonkwekkeegsl--dslsieqinepgrowhceacongegaid 239
                                                    304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTELGESGGKSKSLYGKEGHMGLTLIKFANNSSGLKEAERLAEYLERQDRGRIGWSRAHA 389
                                                                                                                                                                                                                                                                                                                                                               OFRGTDSDIPSSKDSEDSNEDBEEDDEEEDDEDDESDDSQSESDSNSESDTEGSEEB 453
                                                                                            VÁYYAÞCGKKLRÓYÞEVIKYLSRNGIMDISRDNFSFSAKIRVGDFYEARDGÞQEMQWCLL
                                                                                                                                                                                                                                                                          DDDDKDQDESDSDTEGEKTSNKLNKTTSSVKSPSMSLTGHSTPRNLHIAKAPGSAPAALC 513
                                               -----PPMVIIMNTRLDKDDNDKWLGMGNQELLEYFDKY---EALRARHSYGPQGHRGMS 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.5%; Score 182; DB 12; ilarity 20.8%; Pred. No. 0.00018; Conservative 83; Mismatches 190;
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27.0%; Pred. No. 1.2e-06;
ative 40; Mismatches 81
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                                                                                                                                                ---KGLGEDEKD-----
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RESULT 10
US-10-097-340-43
Sequence 43, Application US/10097340
Publication No. US20030087250A1
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                                                      US-10-097-340-43
Query Match
Best Local Similarity
                                                                                                                        SOFTWARE: FastSEQ
SEQ ID NO 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                           PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/323,580 PRIOR FILING DATE: 2001-09-19 NUMBER OF SEQ ID NOS: 363
                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILLING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILLING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILLING DATE: 2001-03-14
PRIOR FILLING DATE: 2001-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                   ORGANISM: Homo sapiens
                                                                                                         ENGTH:
                                                                                                                                                                                                         FILING DATE: 2001-08-10
APPLICATION NUMBER: 60/325,102
FILING DATE: 2001-09-26
                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/324,967
FILING DATE: 2001/09/26
APPLICATION NUMBER: 60/311,732
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Rachel E. MEYERS
Michael MORRISEY
Peter OLANDT
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Karen GLATT
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Robert C. BAST,
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Sebastian HOERSCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosemarie SCHMANDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Karen LU
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Score 178; DB 14;
Pred. No. 0.00019;
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                  Length 1203;
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                US-10-296-115-1265
Sequence 1265, Application US/10296115
Publication No. US20040053248A1
GENERAL INFORMATION:
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 APPLICANT: Hyseq Inc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 121; Mismatches 284;
                                                                                                                                                                                                                                            ----KEMEEFVEEREMLIKDQEKKMEDMKKRHHEEIFDLEKEF-DEALEQLM 615
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                                                                                                                                        913
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FITTLE OF INVENTION: No. US20040053248Alel NU
FILE REFERENCE: 784PCT
CURRENT APPLICATION UNDER: US/10/296,115
CURRENT FILING DATE: 2002-11-18
PRIOR APPLICATION NUMBER: US09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR PILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 1478
SEQ ID NO 1265
LENGTH: 1879
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: misc_feature
LOCATION: (1)...(1879)
OTHER INFORMATION: Xaa = any amino acid or
US-10-296-115-1265
                                                                                                                         RESULT 12
US-09-839-479-71
Sequence 71, Application US/09839479
Publication No. US20020039779A1
GENERAL INFORMATION:
APPLICANT: Jones, Michael H.
APPLICANT: INVENTION: TRANSCRIPTIONAL REGULATOR
TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
FILE REFERENCE: 06501-042002
CURRENT APPLICATION NUMBER: US/09/839,479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1355 LLAEEKNISSKYADERDR-----
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cal Similarity 20.2%;
116; Conservation
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Pred. No. 0.00057;
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                          RESULT 13
US-10-363-616-295
Sequence 295, Application US/10363616
Sequence 295, Application US/10363616
Publication No. US20040044181A1
GENERAL INFORMATION:
GENERAL INFORMATION: NOVEL NUCLEIC AC:
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 09/418,710
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: PCT/JP98/01783
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR APPLICATION NUMBER: JP 9/310027
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
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PRIOR FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 72
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20.1%;
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; pred. No. 0.00079;
94; Mismatches 213;
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                                     POLYPEPTIDES
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Matches Query Match

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GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
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US-10-369-493-43
; Sequence 43, Application US/10369493
; Publication No. US20030233675A1
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CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 09/654,935
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 490
SEQ ID NO 295
LENGTH: 593
TYPE: PRT
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PRIOR APPLICATION NUMBER: US 60/360,039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 GAIDWYNLHPLL----AHARTKGARRVKLHRELAEVLEKDLQMRG-------
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NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 43
LENGTH: 1156
                                                                                                                                                                                   SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 102
LENGTH: 892
TYPE: PRT
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 102, Application US/10205219 Publication No. US20030138803A1 GENERAL INFORMATION:
                                                         Matches 122;
                                                                        Query Match
Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: GB 0118354.0 PRIOR FILING DATE: 2001-07-27 NUMBER OF SEQ ID NOS: 197
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Brooksbank, Robert
APPLICANT: Pinnock, Robert
TITLE OF INVENTION: Identification and Use
FILE REFERENCE: WL-A-018200
CURRENT APPLICATION NUMBER: US/10/205,219
CURRENT FILING DATE: 2002-07-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Warner-Lambert Company
APPLICANT: Lee, Kevin
APPLICANT: Dixon, Alistair
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654
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                                                                        Similarity
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19.9%; Pred. No. 0.00047;
1tive 76; Mismatches 139;
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Search completed: April 6, 2004, 19:40:48 Job time : 49 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
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Minimum
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Pred. No. is the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. ი ი Score Query Match .7 80318 7 110000 7 133120 7 150030 7 150030 7 154923 7 154641 7 174641 7 177529 7 177834 7 177834 7 177834 7 1791391 7 181166 7 181166 7 181391 7 191391 7 193523 101080 101241 101241 126716 152345 180925 170765 Length BB $\begin{smallmatrix} \mathsf{D} & \mathsf{D} & \mathsf{D} & \mathsf{D} \\ \mathsf{D} & \mathsf{D} & \mathsf{D} \\ \mathsf{D} & \mathsf{D} & \mathsf{D} \\ \mathsf{D} & \mathsf{D} & \mathsf{D} \\ \mathsf{D} & \mathsf{D} & \mathsf{D} \\ \mathsf{D} & \mathsf{D} & \mathsf{D} \\ \mathsf{D} & \mathsf{D} & \mathsf{D} \\ \mathsf{D} & \mathsf{D} & \mathsf{D} \\ \mathsf{D} & \mathsf{D} & \mathsf{D} \\ \mathsf{D} & \mathsf{D} & \mathsf{D} \\ \mathsf{D} & \mathsf{D} & \mathsf{D} \\ \mathsf{D} & \mathsf{D} & \mathsf{D} \\ \mathsf{D} & \mathsf{D} & \mathsf{D} \\ \mathsf{D} & \mathsf{D} & \mathsf{D} \\ \mathsf{D} & \mathsf{D} & \mathsf{D} \\ \mathsf{D} & \mathsf{D} & \mathsf{D} \\ \mathsf{D} & \mathsf{D} & \mathsf{D} \\ \mathsf{D} & \mathsf{D} & 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REFERENCE AUTHORS TITLE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	RESULT 1 AX078760
1 Beclin, C., Elmayan, T. and Vaucheret, H. Novel sgs3 plant gene and use thereof	Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	Arabidopsis thaliana	Arabidopsis thaliana (thale cress)		AX078760.1 GI:13158379	AX078760	Sequence 1 from Patent WO0105951.	AX078760 3275 bp DNA linear PAT 22-FEB-2001	

72 72 78 78 84	481 481 541 5601	Qy 301 CCTCCGATCGCCTCACCGCATGCATCTCTCATTTTCTTCTTCTCTCGCTGGAAAA 360 301 CCTCCGATCGCCTCACCGCATGCATTCTGTTCTCTCTTTTTCTTCTCGTGGAAAA 360 361 ATTGCCCTAATGTTCTCGAATGTTTTTGTGCTATA 420 Qy 361 ATTGCCCTAATGTTCTCGAATGTTTTTGTGCTATGTTTTTTTT	21 81 81 41		JOURNAL Patent: WO 0105951-A 1 25-JAN-2001; AVENTIS CROPSCIENCE S.A. (FR); INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (FR) Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/Qualifiers Location/
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TITLE
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                                                    source
                                                                                     AL Submitted (02-APR-1999) Yasukazu Nakamura, Kazusa DNA Research ISBL-LICH (1994) ARR-1999) Yasukazu Nakamura, Kazusa DNA Research ISBL-1994 (1994) Yasukazusa. Sana, Kisarazu, Chiba 292-0812, Japan (E-mail:Ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)

On Sep 15, 2000 this sequence version replaced gi:4589439. Address for correspondence: kaos@kazusa.or.jp

For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MQM1

Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/),

GENSCAN (Chris Burge, MIT, http://CR-081.mit.edu/GENSCAN.html), MREGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brende1, Stanford University, of Denmark, http://www.are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE).

This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is K19M13 and the si
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana genomic
AB025633 BA000015
AB025633.2 GI:10178221
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                                                                      Location/Qualifiers
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me 5, P1
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                                                                                                                        submissions
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SGS

CDS

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KQHSDKAREDWLAAEKLNAEAAKKIIGTTNKDNDIWKLDLHGLHATEAVQALQEELQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(6317. .6428,6508. .6629,6714. .6756,6841. .6932,
7121. .7169,7396. .7466,7550. .7663,7785. .7882,8112. .8181)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (join(8642. .8705,8794. .8863,8978. .9387,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IEGHFTVNRSVSPNRGRSKNAALRSASQEFFGRLDEEGMHCQRTSSRELRNSLQVITG
IGKHSRGQASLPLAVKTFFEDNRYRFDETRPGVITVRPKFRHS"
complement (12417. ..13424)
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unknown protein"
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similar to unknown protein"
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CDS

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SdS

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/ LTAILS ALLONG WISSTAGEMSKEKNVQGGYRPEVEGLVQGLAGTILLASSQDDGGEW
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17943. .18110,18199. .18390)
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DFLAFKNDIQFMKNNSMEGLSAKSVVLNFICQFVLFLYLLDNTSWMILASSGVGVC
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/protein_id="BAA97245.1"
/db_xref="GI:8809704"
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/protein id="BAA97246.1"
/db_xref="GI:8809705"
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26710. .26813,27522. .27765,27943. .28036,28115. .28305,
28385. .28604,28688. .28855,28944. .29092)
/note="gb|AAC97420.1
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/protein_id="BAA97244.1"
/db_xref="GI:8809703"
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IEFWKIGKAMTIEVDRSGMIERLREHDRESYASNKTKEYDDIAIKFLSYVLLLLVIGL
SIYSLAYERHKSWYSWILSSLTSCVYMEGFIMMCPQLFINYKLKSVAHLPWRQMTYKF
LNTIIDDLFAFVIKMPILHRLSVFRDDVIFLIYLYQRWVYPVDKTRVNEFGEGGBET
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Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 2254)

Mourrain, P., Beelin, C., Elmayan, T., Feuerbach, F., Godon, C.,

Mourrain, P., Beelin, C., Lacombe, A.M., Nikic, S., Picault, N.,

Remoue, K., Sanial, M., Vo, T.A. and Vaucheret, H.

Arabidopsis SGS2 and SGS3 genes are required for

posttranscriptional gene silencing and natural virus resistance

cell 101 (5), 533-542 (2000)
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AF239719.1 GI:816402
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Direct Submission
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lin, C., Mourrain, P.,
                                                                                                                             /protein_id="AAF73960.1"
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VDNASEEENDSDALDDSDDDLASDDYSDVSQKSHGSRKQNKWFKKFFGSLDSLSIEQ
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ASVIPCGEIYGQWKGLGEDEXDYEITWPPMVIIMTRLXDDNDKWLGMCNGELLEYF
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FSGGGYRQLYGFLATKODLDIFNQHSQCKTRLKFELKSYQEMVVKELRQISEDNQOLNY
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MDSIKQIHERRDAKEENFEMLQQQERAKVVGQQQQNINPSSNDDCRKRABEVSSTIEF
MDSIKQIHERRDAKEENFEMLQQEKKMEDMKKRHHEEIFDLEKEFDEALEQLMYKHGLHNED
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/product="SGS3"
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chromosome="V"
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/cultivar="Columbia"
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1141 TCTGARGTTGAGAGCAGTGCCACTGGCTATTTGAGAGCCCGAACCCCCCACCGGGGGTT 1200 1896 AGCTGAGATGGGGTTAGATTGAGATGCCTGGGGCAACCCCCGAACCCCCGACCTTTCTTCTTCGAGG 1595 1201 AGCTGAGATGGGTTAGATTGACTGCTGGAACCAGACCAG

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Birect Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M. Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satcou, M., Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A. Arabidopsis Full Length cDNA Clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., W., G., Yuan, S., Chen, H., Cheuk, R., Jones, T., Kim, C.J., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Davis, R.W., Ecker, J.R. and Theologis, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (15-JAN-2003) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted
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                                                         /gene="At5g23570"
92. .1969
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/codon_start=1
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/note="This clone i
                                                                                                                                                                                                                                                                                                         /organism="Arabidopsis thaliana"
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/db_xref="taxon:3702"
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                                                                                                            GATGACGACCTTGCAAGTGATGATTATGACTCGGATGTGAGTCAAAAGAGCCATGGATCA
                                                                                                                                                                                                                                                     GAGGATGATGTGGATAATGCTTCTGAGGAAGAGAATGATTCCGATGCTTTGGATGATTCT
                                                                                                                                                                                                                                                                                    GAGGATGATGTGGATAATGCTTCTGAGGAAGAGAATGATTCCGATGCTTTGGÀTGATTCT 1226
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                         CAGATAAATGAACCACAGAGGCAGTGGCATTGTCCAGCTTGTCAGAACGGACCTGGTGCC
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/note="not present
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Query Match 29.4%; Score 963; DB 6; Length 1878; Best Local Similarity 100.0%; Pred. No. 0; Matches 963; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 963; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 696 ATGAGTTCTAGGGCTGGTCCAATGTCTAAGGAAAAGAACGTTCAGGGTGGTTATAGGCCT 755 LITTLE TO THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE CONTROL OF THE	AC32419:3158381" 3158381" XXSRAGPM XXSRAGPM XXSRAGPM XXSRAGPM XYDDDLA XYDDDLA XYDDDLA XYDDDLA DDSDDDLA	Jalifiers "Arabidopsis thaliana" 'unassigned DNA" caxon:3702"	SOURCE Arabidopsis thaliana (thale cress) ORGANISM Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. REFERENCE 1 AUTHORS Beclin,C., Elmayan,T. and Vaucheret,H. TITLE Novel sgs3 plant gene and use thereof JOURNAL Patent: WO 016951-A 2 25-JAN-2001; AVENTIS CROPSCIENCE S.A. (FR); INSTITUT NATIONAL DE LA RECHERCHE	RESULT 5 AX078761 ACCESSION AX078761 VERSION AX078761 VERSION AX078761 KEYWORDS ACCESSION AX078761 RESULT 5 ACCESSION AX078761 RESULT 5 ACCESSION AX078761 RESULT 5 ACCESSION AX078761 RESULT 5 ACCESSION AX078761 RESULT 5 ACCESSION AX078761 RESULT 5 ACCESSION AX078761 RESULT 5 ACCESSION AX078761 RESULT 5 ACCESSION AX078761 RESULT 5 ACCESSION AX078761 RESULT 5 AX078761 RESULT 5 AX078761	1587 GATTATGAAATTO 983 GATTATGAAATTO 983 GATTATGAAATTO 1647 GATAACGATAAG	Db 743 CAGATAAATGAACCACAGAGGCAGTGGCATTGTCCAGCTTGTCAGAACGAAC
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Spermatophyta; Magnoliophyta; eudicotyledons; Arabidopsis.

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAs: 'RIKEN Arabidopsis Full-Length CDNA'; Seki, M., Narusaka, M., Ishida, Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.
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                                          CCTTGTGGTGAGATTTATGGGCAGTGGAAGGGTTTGGGTGAGGATGAAAAGGATTATGAA 1595
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1548 ATTTATGGGCAGTGGAAGGGTTTGGGTGAGGATGAAAAGGATTATGAAATTGTCTGGCCT 1607	1488 GCTGAAGTTTTAGAAAAGGATCTACAGATGAGAGGCGCATCTGTCATTCCTTGTGGTGAG 1547	1428 CCTCTACTAGCTCATGCGAGGACAAAAGGAGCTAGGCGAGTTAAGCTCCATAGAGAATTG 1487 	/ Match 16.5%; Score 541; DB 8; Length 650; Local Similarity 99.8%; Pred. No. 1.9e-296; hes 591; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	_feature 1650 _note="T-DNA flanking sequence left border"	<pre>/mol_type="genomic DNA" /cultivar="Wassillewskija" /db_xref="taxon:3702" /clone="157008" /clone_lib="Arabidopsis thaliana T-DNA insertion lines"</pre>	<pre>http://genoplante-info.infobiogen.fr). Location/Qualifiers 1650 /organism="Arabidopsis thaliana"</pre>	llable at This sequence lant genomics and	the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a	GASCON Cremieux, 9105/ EVTY CEGEX, FRANCE PCR was performed on DNA from transformants of Arabidopsis thaliana plants from TNDA (Moresilles) The DNA frarment(s) resulting from	Direct Submission Direct Submission Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue	12446565 2 (bases 1 to 650) Balterruic S		Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A. T-DNA integration into the Arabidopsis genome depends on sequences	Eukaryota; Viridiplantae; Streptophyta; Spermatophyta; Magnoliophyta; eudicotyl rosids; eurosids II; Brassicales; Brass 1	AJ528171 AJ528171.1 GI:26796431 left border; T-DNA flanking sequence: Arabidopsis thaliana (thale cress) M Arabidopsis thaliana			1656 AAG 1658 		
,	FEATURES			AUTHORS TITLE JOURNAL	JOURNAL MEDLINE PUBMED REFERENCE	AUTHORS	REFERENCE	VERSION VERSION KEYWORDS SOURCE ORGANISM	DEFINITION	ATH527741 LOCUS	RESIII.T A	Qy 1	Qy 1	Qy 1	Qy 1 Db	Qy 1 Db	Оу 1 Оъ	DЪ	Ωγ 1	Db
organism="Arabidopsis thaliana" /mol_type="genomic DNA"		corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics	plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA detived sequences information to order the	Balzergue,S. Direct Submission Direct Submission Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE DOR was newformed on DNA from transformants of Arabidonsis thaliana	of pre-insertion sites EMBO Rep. 3 (12), 1152-1157 (2002) 2363535 12446565 2 (bases 1 to 45)	Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharry, A. T. DNA integration into the Arabidopsis genome depends on sequences	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	AJ527741.1 GI:26796001 Left border; T-DNA flanking sequence. Arabidopsis thaliana (thale cress) Arabidopsis thaliana	Arabidopais (nailana 1-bun ilanking sequence, ietc boxoer, cione 146F03. Ars9741	ATH527741 45 bp DNA linear PLN 29-MAR-2003		968 GTATGGCTTCCTTGCAACGAAGCAAGATCTGGACATATTCAATCAA	908 GTTAGATAGAATTGCCTGGGGTCAGAAGCGCAGTATGTTTTCTGGAGGTGTTCGCCAACT 1967		.788 TAGAGCACGCCATTCCTATGGTCCACAGGGCCATCGTGGGATGAGTGTTCTGATGTTTGA 1847	.728 GTAGTGGCTCGGCATGGGCAACCAAGAGCTGCTGGAAATACTTCGACAAGTATGAGGCTCT 1787	.668 TTCTGTCTTTACTTCTTTAATTTTTCTCTTGCATTCTACTGATCTTAGAATGTTACATT 1727	181 CCAATGGTCATCATGATACTAGACTGGATAAGGACGATAACGATAAGGTGGAATTC 240	.608 CCAATGGTCATCATGAATACTAGACTGGATAAGGACGATAACGATAAGGTGGAATTC 1667	121 ATTTATGGGCAGTGGAAGGGTTTGGGTGAGGATGAAAAGGATTATGAAATTGTCTGGCCT 180

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AL Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Gardham, L., Grand-Pierre, N., Hafez, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Kanat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Menthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Morman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,
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HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
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1 (bases 1 to 170765)
Birren, B., Nusbaum, C.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Unpublished
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/db_xref="taxon:3702"
/clone="146F03"
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Lander, E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 45;
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Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Myman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Research, 320 Charles Street, Cambridge, MA 02141, USA
On Oct 31, 2002 this sequence version replaced gi:22381142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (31-OCT-2002) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Assembly program: Phrap; version 0.960731
Consensus quality: 169312 bases at least Q40
Consensus quality: 170102 bases at least Q30
Consensus quality: 170102 bases at least Q20
Consensus quality: 170295 bases at least Q20
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Insert size: 170365; sum-of-contigs
Quality coverage: 17.6 in Q20 bases; agarose-fp
Quality coverage: 16.8 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: L18299
Center clone name: 329_L_16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
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76954
78950
79050
92773
92873
150874
                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic_DNA"
/db_xref="taxon:10090"
/clone="RP24-329L16"
                                                                                                                                                                                                                                                                                                           clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76853: contig of 76853 bp in length
76953: gap of 100 bp
78949: contig of 1996 bp in length
79049: gap of 100 bp
92772: contig of 13723 bp in length
92872: gap of 100 bp
150873: contig of 58001 bp in length
150973: gap of 100 bp
170765: contig of 19792 bp in length.
coation/Qualifiers
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vector_side:right"
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                                                                                         150974. .17076
                                                                                                                                                                                                                     /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                               clone_lib="RPCI-24 Male Mouse BAC"
                                                                                                       /note="assembly_fragment"
                                                                                                                                                             note="assembly_fragment"
                                                              'note="assembly_fragment
                                                                                                                                                       .150873
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RESULT 10
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Best Local (
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                                                                                                                                                                                                                                                                                                                         3151 GTTTTTTTTTGGTAAATTTCAT 3173
                                                                              HTG; HTGS PHASE1; HTGS DRAFT.

Danio rerio (zebrafish)

( Danio rerio
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Burton, J.
Direct Su
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1 (bases 1 to 554)

Moran, N.A., Kaplan, M.E., Gelsey, M.J., Murphy, T.G. and Sch Phylogenetics and evolution of the aphid genus Uroleucon mitochondrial and nuclear DNA sequences

Syst. Entomol. 24 (1), 85-93 (1999)
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                                                                                                                                                                                        BX004860 101080 bp
Danio rerio clone BUSM1-144B24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 554)
Moran, N.A., Kaplan, M.E., Gelsey, M.J., Murphy, T.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mitochondrion Uroleucon erigeronensis Uroleucon erigeronensis
                                                                                                                                                                           pieces.
                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (03-APR-1998) Ecology and Evolutionary Biology, University of Arizona, Biological Sciences West, Tucson, Arizona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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                            (bases 1 to 101080)
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Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organelle="mitochondrion"
|mol_type="genomic_DNA"
|db_xref="taxon:87314"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="ND1"
/note="similar to NADH dehydrogenase subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene="ND1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Uroleucon erigeronensis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
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100.0%; Pr
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0; Mismatches
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Aphidiformes;
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4 unordered
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RESULT 12
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Consensus quality: 100257 bases at least Q30
Consensus quality: 100257 bases at least Q20
Consensus quality: 100510 bases at least Q20
Insert size: 1007198; sum-of-contigs
Insert size: 107197; 9.7% error; agarose-fp
Quality coverage: 5.75x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zface@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
------- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (10-DEC-2002) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             coverage: 5.56x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: XGAP4; version 4.5 Chemistry: Dye-terminator; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: dZ144B24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.sanger.ac.uk
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                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                            AAATGAAAACAAAATCAAACTGA 118
                                                                                             AAATGAAAACAAAATCAAACTGA 39769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          be preserved.
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vector_side:right"
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fragment_chain:1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/db_xref="taxon:7955"
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34170: gap of 100 bp
67630: contig of 33460 bp in length
67730: gap of 100 bp
81714: contig of 13984 bp in length
81814: gap of 100 bp
101080: contig of 19266 bp in length.
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Best Local Similarity
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Emm: EMBL; Sw:, SWISSPROT; Tr:, TREMEL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Repeat names beginning 'Dr' were identified by The Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www/Projects/D_rerio/fishmask.shtml
                                                                                                                                                                                                                                                                                                    39751 AAATGAAAACAAAATCAAACTGA 39729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zebrafish DNA sequence from clone BUSM1-132M23 in linkage group 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 101241)
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Danio rerio
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                                                              AC107028
Homo sapiens 3 BAC RP11-547K2 (FBAC Library) complete sequence.
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AC107028
AC107028.5 GI:28006935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="BUSM1-132M23"
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Pred. No.
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Ostariophysi;
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RRS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Banbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Christopullos,C., Chen,R., Dathorne,S.R., David,R., Carron,G., Chen,R., Davis,C., Davy-Carroll,L., Dederich,D.A., David,R., Davis,C., Davy-Carroll,L., Dederich,D.A., David,R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., David,R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., David,R., Chen,R., C.C., Ellaj,C., Escotto,M., Garria,A., Garner,T., Garza,N., Gill,R., Garria,A., Garria,A., Garner,T., Garza,N., Gill,R., Garris,A., Garria,A., Havlak,P., Hawes,A., He,X., Harris,K., Hart,M., Havlak,P., Hale,S., Hamilton,K., Harris,K., Hart,M., Hogues,M., Holloway,C., Harlis,G., Harris,R., Jackson,L., Harris,R., Jackson,A., Hogues,M., Holloway,C., Lewis,L., Liu,W., Johnson,R., Jolivet,S., Juckson,L., Liu,W., Johnson,R., Jolivet,S., Juckson,L., Liu,W., Lewis,L.C., Liu,J., Liu,W., Lewis,L.C., Liu,J., Liu,W., Lewis,L.C., Liu,J., Liu,W., Lewis,L.C., Liu,J., Liu,W., Louder,A., Lucier,R., Luna,R., Martindale,R., 
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Worley.K.C.

Morley.K.C.

Direct Submission

Submitted (14-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One of Molecular and Human Genetics, Daylor College of Medicine, One plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                              Direct Submission
Submitted (30-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                           Submitted (29-APR-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA 4 (bases 1 to 126716)
                           Submitted (02-MAY-2002) Human Genome Sequencing Center, Depa of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Worley, K.C.
Direct Submission
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Baylor Plaza, Houston,
5 (bases 1 to 126716)
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Direct Submission
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Genes and Region of sequences similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (29-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jan 29, 2003 this sequence version replaced g1:20340431.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission

Direct Submission

Direct Submission

Submitted (29-JAN-2003) Human Genome Sequencing of Molecular and Human Genetics, Baylor College of Molecular and Human Genetics, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are esequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of Molecular and Human
Baylor Plaza, Houston,
7 (bases 1 to 126716)
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Submitted (30-MAY-2002) Human Genome Sequencing Center, Departmented (30-MAY-2002) Human Genetics, Baylor College of Medicine,
                                                                                                                                                                                                                                                                                 QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (15-MAR-2003) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA 9 (bases 1 to 126716)
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Direct Submission
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/note="overlaps bases 1.
/function="clone overlap
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                                                                               /clone="RP11-547K2"
                                                                                                    /db_xref="taxon:9606"
/chromosome="3"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 152345)
                                                                                                                                        complete sequence.
BX005128
BX005128.4 GI:375
                                                                               Danio rerio (zebrafish)
Danio rerio
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Zebrafish DNA sequence from
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The following abbreviations are used to associate primary accession rumbers given in the feature table with their source databases: numbers given in the feature table with their source databases: numbers given in the feature table with their source databases: helpining 'New'. sanger ac.uk/Projects/C elegans/wormpep Repeat names beginning 'Or' were identified by the Recon repeat discovery system beginning 'Or' were identified by Rick Waterman (Stephen Johnson lab, WashU). For were identified by Rick Waterman (Stephen Johnson lab, WashU).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Wellcome Trust Sanger Institute
Center code: SC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml
CH211-129H14 is from a CHORI-211 BAC library
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                                                                                                               AC048381.3 GI:8084282
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Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 180925)
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/mol type="genomic DNA"
/db_ref="taxon:7955"
/clone="CH211-129H14"
/clone_lib="CHORI-211"
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Barren,B., Linton,L., Musbaum,C., Lander,B., Burkett,G.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguelavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
Boguelavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Callymore,A., Coke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
Collymore,A., Coke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
Collymore,A., Coke,P., Deverte,M., Graham,L.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Galagan,J., Gardyna,S., Ginde,S., Jones,C., Kann,L., Karatas,A.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,
Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,
Klein,J., LaRocque,K., Lamazares,R., Macdonald,P., Marquis,N.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheters,R.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheters,R.,
McCarthy,M., McEwan,P., Mihova,T., Mirada,C., Mlenga,V., Morrow,J.,
Marphy,T., Naylor,J., Norman,C.H., Peterson,K., Pierre,N.,
O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N.,
O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N.,
Stonger-Thomann,N., Scolanovic,N., Subramanian,A., Talamas,J.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
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RES Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Barne, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Barne, N., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, N., Collins, S., Castle, B., Brown, A., Burkett, G., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Diaz, J.S., Collymore, A., Costle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Collins, S., Ginde, S., Goyette, M., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Horton, L., Garad, P., Domino, M., Ferreira, P., Graham, L., Gage, D., Garad, P., Comino, S., Ginde, S., Goyette, M., Graham, L., Gage, D., Garad, P., Graham, S., Ginde, S., Goyette, M., Graham, L., Karatas, A., Horton, J., Karatas, A., Howland, J.C., Iliev, I., Johnson, R., Landers, T., Lehozky, J., Klein, J., Karatas, A., Landers, T., Lehozky, J., Klein, J., Karatas, A., Landers, T., Lehozky, J., Klein, J., Karatas, A., Landers, T., Lehozky, J., Klein, J., Kockernan, K., McDeeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McDheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McDheeters, R., McCarthy, M., McDan, P., McCarthy, M., McBaga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Marphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Marphy, T., Naylor, J., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., McMan, C., Riley, R., Rogov, P., Rothman, D., Ferre, N., Spancer, B., Schauer, S., Severy, P., Spencer, B., Roy, A., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Thoman, D., Ye, W.J., Vell, R., Vo, A., Wilson, B., W., Myman, D., Ye, W.J., Vo, A., Wilson, B., W., Myman, D., Ye, W.J., Vo, A., Wilson, B., Markett, G., Myman, D., Ye, W.J., Vo, A., Wilson, B., Markett, G., Markett, G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (24-AUG-2002) whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 25, 2000 this sequence version replaced gi:7770638. All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                              Center clone name: 547 K 2

------ Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 158029 bases at least Q40
Consensus quality: 168695 bases at least Q20
Consensus quality: 173285 bases at least Q20
Consensus quality: 173285 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIR Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: L9685
Insert sizē: 183000; agarose-fp
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RP11-547K2
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NOTE: This is a 'working draft' sequence. It currently consists of 37 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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1110: gap of 100 bp
27487: contig of 1377 bp in length
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g of 2873 bp in length
f 100 bp
g of 2058 bp in length
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f 100 bp
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g of 1404 bp in length
f 100 bp
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                            100 bp 7 of 6072 bp 106 6270 bp 100 b
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Search completed: April Job time: 8467.3 secs
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116971: contig of 7986 bp in length
117071: gap of 100 bp
126718: contig of 9647 bp in length
126818: gap of 100 bp
137354: contig of 10536 bp in length
137454: gap of 100 bp
146943: contig of 9489 bp in length
1477043: gap of 100 bp
157785: contig of 10742 bp in length
157885: gap of 100 bp
180925: contig of 23040 bp in length.
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                           AAS46448
ABN80176
ADA02738
ADB72476
ADC52596
AAC52596
AAC54974
ABC78073
AAC60012
ABQ34916
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AAF25371
AAF25371
ABK40041
ABN80100
ABL33241
ABL32509
ABL325031
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Aaf25373 Genomic s
Aaf25374 Nucleotid
Aaf25372 PCR prime
Aaf25371 PCR prime
Aaf25371 PCR prime
AbA40041 Human che
Abh80100 Human imm
Ab132031 Human imm
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Aac60012 Human bre
Aac60012 Human sce
Abg34916 Oligonucl
Abf32427 Oligonucl
Aaf12773 Aspergill
Abg52242 Oligonucl
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σ	0	9	σ	σ	4	7	7	9	9	v	7	4	Φ	9	9	9	σ	σ	σ	4	N
AAS61413	ABL70450	ABK31481	ABL34150	ABL32823	AAS46376	ABZ10216	ABZ10070	ADB54169	ADB54297	ABA20651	ACA23079	AAL25105	ABT07654	ADD48892	ADD47852	ADD47853	ABK48300	ABQ30108	ABQ30109	AAH93017	AAX27594
Aas61413 Human gen	Abl70450 Chemicall	Abk31481 Signal tr	Abl34150 Human imm	Abl32823 Human imm	Aas46376 Tumour su	Abz10216 Haematopo	Abz10070 Haematopo	Adb54169 Pretreate	Adb54297 Pretreate	Aba20651 Human ner	Aca23079 Prokaryot	Aal25105 Human bre	Abt07654 Human bre	Add48892 Rat gene	Add47852 Rat gene	Add47853 Rat gene	Abk48300 Human inh	Abq30108 Oligonucl	Abq30109 Oligonucl	Aah93017 Human inf	Aax27594 Nucleotid

ALIGNMENTS

AAF25373;

AAF25373 standard; DNA; 3275

ВP

15-MAY-2001

(first entry)

Genomic sequence of the Arabidopsis SGS3 gene

RESULT 1
AAF25373
ID AAF25373
XX AAF25373
XX AAF2
XX AAF2
XX SGS3
XW Vira
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XX S exon exon exon 16-JUL-1999; 99FR-00009417. 26-JAN-2000; 2000FR-00001006. SGS3 gene; post-transcriptional inactivation; RNA degradation; viral resistance; resistance; fatty acid content; protein content; ss. (AVET) AVENTIS CROPSCIENCE SA. (INRG) INST NAT RECH AGRONOMIQUE. 13-JUL-2000; 2000WO-FR002052 25-JAN-2001. WO200105951-A2. intron intron exon intron intron exon Arabidopsis thaliana. /*tag= a 1659. 1731 /*tag= . 2023 /*tag= . c 2024. 2134 /*tag= . d 2135. 2379 /*tag= e 2380. 2481 /*tag= . 64 /*tag= . 64 /*tag= . 2481 /*tag= . 2481 /*tag= . 2481 /*tag= . 2481 /*tag= . 2481 Location/Qualifiers 696. .1658 .1658

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                                                                                  New SGS3 gene from Arabidopsis thaliana, useful for increasing virus resistance in plants and, when inhibited, for increasing transgene
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26-JAN-2000;
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                                                                                          PCR primers AAF25371-72 were used to amplify cDNA encoding an Arabidopsis thaliana SGS3 polypeptide. The SGS3 gene is essential for post-transcriptional inactivation (degradation of RNA) and for resistance to viruses. Overexpression of SGS3 results in plants with increased viruses, while inactivation of SGS3 in transgenic plants resistance to viruses, while inactivation or SGS3 in transgenic plants (e.g. by expressing antisense RNA, by mutation or by homologous (e.g. impart resistance (to herbicide, insects or pathogens), alter may e.g. impart resistance (to herbicide, insects or pathogens), alter contents of essential fatty acids or proteins, or is pharmaceutically active, e.g. an immunoglobulin or interferon
                                                                                                                                                                                                                                          New SGS3 gene from Arabidopsis thaliana, useful for increasing virus resistance in plants and, when inhibited, for increasing transgene expression.
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26-JAN-2000; 2000FR-00001006.
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Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tu cytostatic; ALDH6; CYP11A; CYP11B1; CYP3A3; DPYD; EPHX2; OCLN; TX UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New SGS3 gene from Arabidopsis thaliana, useful for increasing virus resistance in plants and, when inhibited, for increasing transgene
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26-JAN-2000; 2000FR-00001006.
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                                                                                                                Human chemically pretreated gene sequence #62 strand 1.
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Query Match Best Local S Matches 22

Similarity

Conservative 0;

0.7%;

Score 22; DB 6; Length 6136; Pred. No. 12;

Mismatches

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RESULT 6

ABN80100;

15-JUL-2002

(first entry

ABN80100 standard; DNA; 6301 BP

Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis; heart disease; epilepsy; histone deacetylation; muscular dystrophy; dwarfism; single nucleotide polymorphism; SNP; cytosine methylation;

Human chemically modified disease associated gene SEQ ID NO 117.

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The invention relates to a nucleic acid comprising a sequence at least 18 CC bases in length of a segment of the chemically pretreated DNA of genes CC associated with pharmacogenomics according to one of the sequences of the Genes ALDH6 (NM 000693), CYP11A (NM 000781), CYP11B (NM 000781), CYP1B1 (NM 000781), CYP1B1 (NM 000781), CYP1B1 (NM 000781), CYP1B1 (NM 0019079), CCLN (NM 0019076, and NM 017460), DPYD (NM 001010), EPHX2 (NM 001979), CCLN (CC (NM 001990), NM 019901, NM 019902, NM 019862, NM 019898, NM 019899) and CC (NM 019900, NM 019901, NM 019902, NM 019862, NM 019898, NM 019899) and CC treatment to convert cytosines (but not methyl-cytosines) into uracils. CC peptide nucleic acid (PNA)-oligomer, Comprising in each case at least one CC base sequence having a length of 9 nucleotides which hybridises to or is cidentical to a chemically pretreated DNA of genes associated with CC pharmacogenomics and their complements, arranged in an array for CC analysing diseases associated with the methylation state (CpG) and/or detecting SNPs (single nucleotide polymorphisms) of the 87 sequences. The CC cligomers may also be used as PCR primers. The set of 87 nucleic acids cand their complement is useful for diagnosis and therapy of solid CC and their complement. Note: The sequence data for this patent did cnot form part of the printed specification, but was obtained in CC electronic format directly from WIPO at CC format dir
Sequence 6136 BP; 1661 A; 69 C; 1415 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer.
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01-SEP-2000; 2000DE-01043826
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RESULT 7
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01-SEP-2000;
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of a segment of chemically pretreated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA (II) of genes associated with development selected from 87 genes listed in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-130908/17.
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                          Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                               Human immune system associated gene SEQ ID NO: 1214
                                                                                                                                                                                                                                                                                                         ABL33241 standard; DNA;
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22; Conserv
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2000DE-01043826.
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RESULT 8
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    methylation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              macular degeneration, arteriosclerosis, anaemia, cancer, acute mye leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
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                                                                                                                                                                                                                                                                                                                      antiarteriosclerotic; antianaemic; cytostatic; nootropic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; antiarteriosclerotive; anti-HIV; anticonvuleant; ophthalmological; neuroprotective; anti-HIV; antidiabetic; antipsoriatic; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immune system
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                                                                                                                                                                                                           sapiens.
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2000DE-01043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA; 6048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Berlin
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Pred. No.
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bowel disease; gene;
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bowel disease;
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02-JUL-2001; 2001WO-EP007537

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Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    macular degeneration, arteriosclerosis, anaemia, cancer, acute mye leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; immune system disease; antiarteriosclerotic; antianae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL32031 standard;
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                                                                                                                                                                                         30-JUN-2000; 2000DE-01032529
01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                                                                02-JUL-2001; 2001WO-EP007537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurofibromatosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immune
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                                               WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                          Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention provides a number of human immune system associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rheumatoid arthritis;
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Pred. No.
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tis; psoriasis; bowel disease; gene;
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Nucleic acid comprising fragment of chemically modified gene, useful

for

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RESULT 10
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Matches 21
                                                                                                                                                                                                                                                                                         Fragments of chemically modified genes associated with tumor suppressor genes and oncogenes, useful in designing primers and probes for analyzin diseases associated with cytosine methylation state e.g. cancer.
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06-APR-2000; 2000DE-01019058

07-APR-2000; 2000DE-01019173

30-JUN-2000; 2000DE-01032529

01-SEP-2000; 2000DE-01043826
                           complementary to (Ss). The nucleic acid may be a peptide nucleic aci oligomer (PNA) of at least 9 nucleotides and may form part of a set
                                                                     The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 at 500 are missing from the sequence listing) sequences (Ss) and sequences
                                                                                                                                                                                                                                         Claim 1;
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tumour; CpG d:
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     the cytosine methylation state
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polymorphism; SNP;
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ABN80176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis; heart disease; epilepsy; histone deacetylation; muscular dystrophy; dwarfism; single nucleotide polymorphism; SNP; cytosine methylation; antidiabetic; cytostatic; anticonvulsant; ds.
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The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA (I) least 18 bases in length of a segment of chemically pretreated in of genes associated with development selected from 87 genes listed in specification such as ACCPN, ADFN, or AFD1 and comprising one of 350 sequences (ABN79984-ABN80333) or their complements. The invention is
                                                                                                                                                       Novel nucleic acid useful for diagnosis and therapy of diseases associated with development genes such as diabetes, comprises a sequence of a segment of chemically pretreated DNA of genes associated with
                                                                                                                                                                                                                                                                                                                                    30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                WPI;
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                                                                                                        Claim 1; SEQ ID NO 193;
                                                                                                                                                                                                                                                                                                 (EPIG-)
                                                                                                                                          development.
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                                                                                                                                                                                                                                                                 Piepenbrock
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2000DE-01043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; carcinoma associated; oncogene; carcinoma; cancer; breast; prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human CCND2 carcinoma associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA02738;
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The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a invention also encompasses expression vectors and host cells comprising CA nucleic acid or binds to the protein, and a biochip comprising CA nucleic acid or binds to the protein, and a biochip comprising CA nucleic acid or binds to the protein, and a biochip comprising CA nucleic acid or organism oncogenic retroviruses, which insert into the genome of the host organism oncogenic retroviruses, which insert into the genome of the host organism oncogenic trans-acting viral genes, meaning that cancer incidence is a pathogenic trans-acting viral genes, meaning that cancer incidence is a pathogenic trans-acting viral genes, meaning that cancer incidence is a pathogenic trans-acting viral genes, meaning that cancer incidence is a pathogenic trans-acting viral genes, meaning that cancer incidence is a pathogenic trans-acting viral genes, meaning that cancer incidence is a pathogenic trans-acting viral genes of proviral integration into host
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                                                                                                                                                                                                                                                                                                             New recombinant nucleic acid encoding carcinoma useful for preparing compositions for treating c
                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-587068/55
                                                                                                                                                                                                                                                                                                                                                                                                                      Morris
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SAGR-) SAGRES
                                                                                                                                                                                                                                                                            Claim 1;
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                                                                                                                                                                                                                                                                            SEQ ID NO 1256;
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                                                                                                                                                                                                                                                                                                                              a associated protein, carcinomas.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-MAR-2001; 2001US-00798586.
23-OCT-2001; 2001US-00004113.
08-NOV-2001; 2001US-00052482.
30-NOV-2001; 2001US-00997722.
20-DEC-2001; 2001US-00034650.
                                                                                                                                                                               nucleotide sequence selected from any of the 660 sequences fully defined in the specification. A polynucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polypeptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a human gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 304; 2304pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancers,
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                                                                                                                                 Sequence 52302 BP;
                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel recombinant nucleic acid comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant nucleic acid, useful for treating carcinomas,
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            Score 21; DB ;; Pred. No. 33; 0; Mismatches
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Best Local S
Matches 21
             Hybridisation assay; genetic mapping; protein identification; signal transdu
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                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the carcinoma-associated (CA) genes, u
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                                                        Arabidopsis thaliana DNA fragment SEQ ID NO: 71849.
                                                                                      18-OCT-2000
                                                                                                                                              AAC52596
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Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T.,	1 (bases 1 to 693)	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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Fax: 301 838 0208 Email: at@tigr.org For addtional information, see http://www.tigr.org/tdb/at/at.html	polymorphisms Unpublished (2000) Contact: Xiaoying Lin The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA	Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M. Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based

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Unpublished (2000)
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Unpublished (2000)
Contact: Xiaoying Lin
Contact: Xiaoying Lin
Por 12 Medical Center Dr., Rockville, M
9712 
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Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M. Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
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<u>AAAGAGCCATGGATCACGAAAGCAGAATAAGTGGTTCAAAAAGTTCTTTGGCAGCTTGGA</u>
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/mol_type="genomic DNA"
/strain="LANDSBERG ERECTA"
/db_xref="taxon:3702"
/clone="LEREM21"
/clone_lib="LEREM2"
/clone_lib="LERE"
/clone_lib="LERE"
/strain="Leaf; Vector: pUC19JK; Total genomic DNA was sheared to 0.6-0.8 Kbp before ligation."
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JOURNAL
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Matches 521;
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Best Local Similarity
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An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998).cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3-1-1 Koyadai, Tsukuba,
Tel: 81-298-36-4359
Fax: 81-298-36-9060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Large scale analysis of Arabidopsis full-length cDNA (2002b) Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
Oono,Y., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
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Plant Functional Genomics Research Group
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AU236368.1 GI:19875537
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AU236368 RAFL14
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                                                                                                                                                                                                                                                                                                                                                    TATAGGCCTGAGGTTGAACAGTTGGTTCAAGGTTTGGCAGGGACGAGACTGGCTTCTTCA
                         GGCAATGGTCGGGGCATTCAAGCTAACATATCTGGTCGGGGACCGAGCGTTGAGCAGAAAG
                                                                                                                                                                                                                                                                                    CAAGATGATGGAGGAGAGTGGGAGGTCATTTCCAAGAAGAACAAGAACAAACCAGGAAAC
                                                                                                                                                                                                                                                                                                                                                                                                             GTTGTAAAAATGAGTTCTAGGGCTGGTCCAATGTCTAAGGAAAAGAACGTTCAGGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTGTAAAAATGAGTTCTAGGGCTGGTCCAATGTCTAAGGAAAGAACGTTCAGGGTGGT
GGCAATGGTCGGGGCATTCAAGCTAACATATCTGGTCGGGGACGAGCGTTGAGCAGAAAG
                                                                                                                                                             ACTTCTGGAAAAACTTGGGTTTCTCAGAATTCGAATCCTCCTAGAGCTTGGGGTGGTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RAFL14-93-K05"
/tissue_type="root"
/lab_host="DH10B"
/clone_lib="RAFL14"
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/db_xref="taxon:3702"
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Pred. No. 1.1e-249;
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Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M.
Genomic survey sequencing of Landsberg erecta ecotype of Genomic survey sequencing of Landsberg erecta ecotype of Genomic survey sequencing of Landsberg erecta ecotype of Genomic survey sequences and identification of sequence-based
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Tel: 301 838 0200
Fax: 301 838 0208
Email: at@tigr.org
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LERGX20TF LERG Arabidopsis thaliana
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Class: shotgun
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The Institute for Genomic Research
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                    CTGGCTTCTTCACAAGATGATGGAGGAGAGAGGAAGAACAAGAAC
                                                                                             GTTCAGGGTGGTTATAGGCCTGAGGTTGAACAGTTGGTTCAAGGTTTGGCAGGGACGAGA
                                                                                                                                                            TGGTGGCTATAGGTTGTAAAAATGAGTTCTAGGGCTGGTCCAATGTCTAAGGAAAAGAAC
                                                                                                                                                                                                                              TGTTATAACTTCACGTTCATGTGTGGATTTTTGAGATTTTTGGTAGTGACTGTGGGTTTTCTT
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CTGGCTTCTTCACAAGATGATGGAGGAGGTGGGAGGTCATTTCCAAGAAGAACAAGAAC
                                                                    GTTCAGGGTGGTTCTAGGCCTGAGGTTGAACAGTTGGTTCAAGGTTTGGCAGGGACGAGA
                                                                                                                                      TGGTGGATATAGGTTGTAAAAATGAGTTCTAGGGCTGGTCCAATGTCTAAGGAAAGAAC
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                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="LERG"
/note="Organ: Leaf; Vector: pUC19JK; Total
sheared to 0.4-0.7 Kbp before ligation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Arabidopsis thaliana"
|mol_type="genomic DNA"
|strain="LANDSBERG ERECTA"
                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:3702"
clone="LERGX20"
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                                                                                                                                                                                                                                                                                               15.4%;
99.7%;
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Pred. No. 3.8e-241;
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RESULT 5
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TITLE
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                                                       Matches 451;
                                                                                  Query Match
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                                                       Local Similarity 100 hes 451; Conservative
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Arabidopsis thaliana (thale cress)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana genome survey sequence T7 end of BAC F8G21 of
IGF library from strain Columbia of Arabidopsis thaliana, genomic
                                                                                                                                                                                                                                                                   Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               survey sequence.
AL084227
AL084227.1 GI:5
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                                                                                                                                                                                                                                                                                                              Genoscope
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                                                                                                                                                                                 /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia"
                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                            /clone="F8G21"
/clone_lib="IGF"
/note="end : T7"
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                                                                    13.8%;
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Pred. No.
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                                                                                  Length 457;
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RESULT 6
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AU227277
AU227277.1 GI:
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Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Akiyama, K., Enju, A., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA Unpublished (2002)
                                                                                                                                                                                                                                                                                                               Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998).cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and Sall. This
clone is in a modified pBluescript vector. Please visit our web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
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Plant Functional Genomics Research Group
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AU227277 RAFL14 Arabidopsis
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                                                                                                                                                                                                                                                                                    (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
/tissue type="root"
/lab_host="DH108"
/clone_lib="RAFL14"
/note="Site_1: BamHI; Site_2: SalI"
                                                                                                           /clone="RAFL14-93-K05"
                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:3702"
                                                                                                                                                                                      organism="Arabidopsis"
                                                                                                                                                                                                                                      Location/Qualifiers
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KEYWORDS
SOURCE
ORGANISM
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VERSION
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                                                                                                                                                                                                                                                              Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D. Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nuyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Carpio, A., Murry, L., Turner, C., Krikorian, S., Elder, L. and
                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 548)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI999551 548 bp mRNA linear EST 08-SI 701556368 A. thaliana, Columbia Col-0, rosette-3 Arabidopsis thaliana cDNA clone 701556368, mRNA sequence. AI999551
                                                                                                                                          4633 World Parkway Circle, St. Louis, Tel: 877-577-2733
                                                                                                                                                                                                                    Arabidopsis thaliana Gene Expression MicroArray
Unpublished (1999)
                                                                                                                                                                         Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI999551.1 GI:5846456
                                                                                                                                                                                                     Contact: David Smoller, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATCTAAGGAAGCATTAAGTTCTTGTGAC 3125
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                                                                                                                           314-427-3324
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                                                                                          service@genomesystems.com
Location/Qualifiers
/db_xref="taxon:3702"
/clone="701556368"
                             /mol_type="mRNA"
/cultivar="Columbia Col-0"
                                                           organism="Arabidopsis thaliana"
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
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Best Local Similarity
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 380)
Asamiru, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV525508 Arabidopsis thaliana aboveground organs two to six-week old Arabidopsis thaliana cDNA clone APD25d02R 5', mRNA sequence AV525508
                                                                                                                                                                                       The First Laboratory for Plant Gene Research Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AV525508.1 GI:8685036
EST.
                                                                                                                                                                                                                                                       Contact: Erika Asamizu
                                                                                                                       Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                                                                                                                                        10907847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (thale cress)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAATTTTTAGTAGACGGATCTAAGGAAGCATTAA 3114
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/clone lib="A. thaliana, Columbia Col-0, rosette-3"
/note="Vector: pSPORT; Site 1: Notl; Site 2: Sall; cDNA
library was derived from untreated rosette tissue from
Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks.
Plants were grown in 1:1:1 peat moss/vermiculite/perlite
soil at 22 deg. C +/-3 deg. C under constant light, and
watered with fertilizer. cDNA synthesis was initiated
using a Notl-oligo(dT) primer. Double-stranded cDNA was
blunted, ligated to Sall adaptors, digested with Notl,
size-selected, and cloned into the Notl and Sall sites of
the pSPORT vector."
                                                                                          Location/Qualifiers
organism="Arabidopsis/mol_type="mRNA"
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        9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
Email: rounsley@tigr
                                                                                                        (bases 1 to 290)
(Chases 1 to 290)
(Rounsley,S.D., Suh,E.J., Wible,C., Golden,K., Shatsman,S., Choi, Yu,K., Akinretoye,B., Shen,K., Goonasekaram,S., Militscher,J., Adams,M.D. and Venter,J.C.
A BAC End Sequence Database for Identifying Minimal Overlaps in A BAC End Sequence Sequencing. Update 4
Unpublished (1998)
Other GSSS: F27C8TFC
Contact: Steve Rounsley
                                                                                                                                                                                                                                                    Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; Brassicaceae; Arabidopsis.
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AQ010650.1 GI:3165927
GSS.
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F27C8TRC IGF Arabidopsis
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primer: M13 Reverse
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/db_xref="taxon:3702"
/clone="ApD25d02R"
/tissue_type="aboveground organs"
/dev_stage="two to six-week old"
/clone_lb="Arabidopsis thaliana aboveground organs two six-week old"
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Pred. No. 3.1e-153;
0; Mismatches 1;
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thaliana genomic clone F27C8, genomic
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                                                                                                                                                                                                                                       1 (bases 1 to 523)
Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M. Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                            polymorphisms
Unpublished (2000)
Unpublished (2000)
Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                              Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGCAGTGCCACTGGCTATTTGGAGGCCGAACGCCTCCACCGGGAGTTAGCTGAGATGGG 1907
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                                                                                               Email: at@tigr.org
For addtional information,
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/clone lib="IGF"
/clone="Vector: BeloBACII; S:
produced by Thomas Altmann"
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/strain="Columbia"
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'clone="F27C8"
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
                                              ocation/Qualifiers
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Pred. No. 1.3e-133;
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    Li,Y.,
Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL945644 536 bp DNA linear GSS 30-NOV Arabidopsis thaliana T-DNA flanking sequence GK-290H04-015353,
                                                                                                                                                                                                                                               and
                                                                                                                                                                                                                                                                                                                                                                                                         AL945644.1
GSS.
                                                                           Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) A new Arabidopsis thanking sequence tag based reverse genetics
                                                                                                                                                                                  A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
                                                                                                                                                                                                                                                              Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H.
                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic survey sequence.
                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
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(bases 1 to 536)
Y., Rosso,M., Strizhov,N. ect Submission
                                                                                                                                                                                                                                               Weisshaar, B.
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/note="Organ: Leaf; Vector: pUC19JK; Total
sheared to 0.6-0.8 Kbp before ligation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="LANDSBERG ERECTA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="LEREM21"
                                                                                                                                                                                                                                                                                                                                                                                                                              GI:24402266
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No. 3.8e-125;
                         and
                         Weisshaar, B.
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Ś 멍 Ś В δ 밁 S 밁 á 밁 Š 밁 Ś 밁 5

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ACCESSION
VERSION
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AV566465/c
LOCUS
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TITLE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AV566465 Arabidopsis thaliana gr.
thaliana cDNA clone SQ244b06F 3'
Contact: Erika Asamizu
The First Laboratory for Plan
Kazusa DNA Research Institute
                                                                                                                                                                            1 (bases 1 to 619)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thalian
of 12,028 non-redundant expressed sequence tags from
size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mgo.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone MQM1. The sequences are generated at the MPI for plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German
                                                                                                               10907847
                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                                    Spermatophyta; Magnoliophyta; eudicotyledons; corosids; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AV566465.1 GI:8737917
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ilarity 100.0%;
Conservative (
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/clone=lib="Arabidopsis thaliana T-DNA insertion lines"
/clone lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
plants (T1) which were transformed with the T-DNA from
yestor pAC161. The lines contain one or more T-DNA
T-DNA from the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the procession of the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          processed for submission. T-DNA derived sequences were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="Columbia 0"
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Pred. No. 1.4e-104;
0; Mismatches 0;
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FEATURES
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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; care eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                         Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R. A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                      Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                        Arabidopsis Genome
Unpublished (2001)
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/clone_Tib="Arabidopsis_thallana_green_siliques_Columbia"
/note="Vector: pBluescriptII_SK-; Site_1: EcoRI; Site_2:
XhoI"
                                                                                                                                                                           ecker@salk.edu
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/mol_type="mRNA"
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/mol_type="genomic_DNA"
/strain="Columbia 0"
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Arabidopsis thaliana T-DNA flanking
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                                                                                  Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It midicates an insertion within the locus defined by clone MQM1. The sequences are generated at the MPI for Plant Breeding Research in sequences are generated at the project. GABI-Kat is part of the German the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:

availability can be found at:

http://www.mpiz-koeln.mpg.de/GABI-Kat/.

Location/Qualifiers
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                                                                                                                                                                                                                                                        Submitted (01-JUL-2003) Weisshaar B., Max-Planck-Institut fuer
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/note="pCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
each of the resultant fragment for each line was
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
the site of insertion. Jetails of the protocols.html"
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
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(GABI-Kat)
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BH169457
                                                                                                                                                                                                                                                                                                            Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 197)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zhmmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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                                                                                                                                                                                                                                                                                      ecker@salk.edu
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/clone="SALK_001394"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
                                                                       /mol_type="genomic DN/
/strain="Columbia 0"
/db_xref="taxon:3702"
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Pred. No. 2.1e-73;
0; Mismatches 1;
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each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Ś Matches 153; Query Match Local 745 Similarity GTTATAGGCCTGAGGTTGAACAGTTGGTTCAAGGTTTGGCAGGGACGAGACTGGCTTCTT Conservative 100.0%; 4.7%; 0 Score 153; DB 28; Pred. No. 8.3e-65; Mismatches Length 197; Indels 0; Gaps 804

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Ś 밁 밁 805 5 CACAAGATGATGGAGGAGAGTGGGAGGTCATTTCCAAGAAGAACAAGAACAAACCAAGAA GTTATAGGCCTGAGGTTGAACAGTTGGTTCAAGGTTTGGCAGGGACGAGACTGGCTTCTT CACAAGATGATGGAGGAGAGTGGGAGGTCATTTCCAAGAAGAACAAGAACAAACCAGGAA 120 864 60

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ACACTTCTGGAAAAACTTGGGTTTCTCAGAATT

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Maximum DB
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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4 US-08-975-19-789-27

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1 US-09-484-1075A-6

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Sequence 31, Appli
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US-09-112-584-1/c
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	Seguence 120, App	Sequence 120, App	Sequence 49, Appl	Sequence 49, Appl	Sequence 49, Appl	Sequence 49, Appl	Sequence 25, Appl	Sequence 2618, Ap	Sequence 15, Appl	Sequence 8, Appli	Sequence 14, Appl	Sequence 13, Appl	Sequence 10, Appl	Sequence 7, Appli	Sequence 6, Appli	Sequence 12, Appl	Sequence 11, Appl	Sequence 1, Appli

ALIGNMENTS

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TITLE OF INVENTION: ESCHERICHIA COLI CSRB GENE, RN
TITLE OF INVENTION: THEREBY, AND METHODS OF USE T
FILE REFERENCE: 316082002001
CURRENT APPLICATION UMMBER: US/09/736,734
CURRENT FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 09/112,584
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: 60/052,372
PRIOR APPLICATION NUMBER: 60/052,372
PRIOR APPLICATION NUMBER: 10
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LENGTH: 654
; TYPE: DNA
; ORGANISM: Escherichia coli
US-09-112-584-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Romeo, Tony
APPLICANT: University of No. 6228638th Texas
APPLICANT: University of No. 6228638th Texas
TITLE OF INVENTION: THE ESCHERICHIA COLI CSRB GENE, RNA ENCODED THEREBY,
TITLE OF INVENTION: AND METHODS OF USE THEREOP
FILE REFERENCE: 31608200200
CURRENT APPLICATION NUMBER: US/09/112,584
CURRENT FILING DATE: 1998-07-09
EARLIER APPLICATION NUMBER: US 60/052,372
EARLIER APPLICATION NUMBER: US 60/052,372
EARLIER FILING DATE: 1997-07-11
NUMBER OF SEQ ID NOS: 10
SOPTWARE: Patentin Ver. 2.0
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Patent No. 6228638
GENERAL INFORMATION:
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Best Local Similarity
Matches 20; Conserv
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US-09-615-192A-109
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US-09-615-192A-109/c
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                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Materials and Methods for TITLE OF INVENTION: Modification of Plant Lix FILE REFERENCE: 11000.1003c2

CURRENT APPLICATION NUMBER: US/09/169,789

CURRENT FILING DATE: 1998-10-09

EARLIER APPLICATION NUMBER: US 08/975,316

EARLIER FILING DATE: 1997-11-21

EARLIER APPLICATION NUMBER: US 08/713,000

EARLIER FILING DATE: 1996-09-11

NUMBER OF SEQ ID NOS: 185
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                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 109
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APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 109
LENGTH: 481
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APPLICANT: Bloksbe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.0%; Matches 20; Conservative (
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    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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IIILE OF INVENTION: Modification of Plant Lignin Content
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ORGANISM: Escherichia coli
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                                                                                                                           ORGANISM: Eucalyptus grandis
                                                                                                                                                                          LENGTH: 481
TYPE: DNA
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100.0%; Pred. No.
    0.6%;
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    Score 19;
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    DB 4;
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Length 481;
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US-09-615-192A-27/c
; Sequence 27, Application US/09615192A
; Patent No. 6410718
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                                                                                                                                                                                                                                                                                                                                                                      US-08-975-316-27
                                                          GENERAL INFORMATION:
APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilka
                                                                                                                                                                                                                                                                                             Matches
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              TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin FILE REFERENCE: 11000.1003c4U
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CURRENT APPLICATION NUMBER: US/09/615,192A
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 495 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 206-269-0565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/713,000
FILING DATE: September 11, 1996
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 495 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: SLEATH, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Law Offices of Ann W. Speckman STREET: 2601 Elliott Avenue, Suite 4185
                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 206-269-0563
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CURRENT FILING DATE:

2000-07-12

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CURRENT APPLICATION NUMBER: US/09/169,789
CURRENT FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 08/975,316
EARLIER FILING DATE: 1997-11-21
EARLIER APPLICATION NUMBER: US 08/713,000
EARLIER FILING DATE: 1996-09-11
NUMBER OF SEQ ID NOS: 185
SOPTWARE: FASUSEQ for Windows Version 3.0
SEQ ID NO 27
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Best Local Similarity
"hes 19; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-169-789-27
                                                                                                                                                                                                                                                                 RESULT 8
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SEQ ID NO 27
LENGTH: 495
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Matches
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Patent No. 5589341
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                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Materials and Methods TITLE OF INVENTION: Modification of Plant FILE REFERENCE: 11000.1003c2
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APPLICANT: Havukkala,
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mes 19; Conserv
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               INVENTION:
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LAURENSON, PALTICIA
HERSKOWITZ, Ira
LI, Joachim J
LI, Joachim J
GAVIN, Kimberly
VENTION: ORIGIN OF REPLICATION COMPLEX GENES
                                                                                                        RINE, Jasper
FOSS, Margit
                                                                                                                                            BELL, Stephen P
KOBAYASHI, Ryuji
                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                        STILLMAN, Bruce
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                                                                                              Francis J
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100.0%; Pred. No.
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00.0%; Pred. No.
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24;
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Lignin Content
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                             APPLICANT: APPLICANT:
                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                           TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                               APPLICANT:
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TELECOMMUNICATION INFORMATION:
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NAME: Osman Ph.D., Richard Aron
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APPLICATION NUMBER: US,
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                             APPLICANT:
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                                                                                CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                   ZIP: 94111-4187
                                                                 COUNTRY:
                                                                                                                 STREET:
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les 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
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                                                                                                                 4 Embarcadero Center,
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                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : (415) 494-8700
(415) 494-8771
                                                                                                                                                                            GAVIN, Kimberly
JENTION: ORIGIN OF REPLICATION COMPLEX GENES
                                                                                                                                                                                                                                                                                                        BELL, Stepnen r
KOBAYASHI, Ryuji
                                                                                                                                                                                                                                                                                            RINE, Jasper
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                                                                                                                                                                                                                                                           FOSS, Margit
McNALLY, Francis
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277..1365
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                                                                                                                                TEST, ALBRITTON & HERBERT
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; ORGANISM: Oryza sativa
US-09-377-557-9
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                                                                        RESULT 11
US-09-041-075A-4
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                       SEQ ID NO 9
                                                                                                                                                                                                                           Query Match
                           GENERAL INFORMATION:
                                        Sequence 4, Applic
Patent No. H002022
                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/377,557
CURRENT FILING DATE: 1999-08-19
EARLIER APPLICATION NUMBER: 60/099,493
EARLIER FILING DATE: September 8, 1998
NUMBER OF SEQ ID NOS: 20
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Layo O.
APPLICANT: Orozco, Emil M. Jr.
APPLICANT: NOVENTION: Amino Acid Decarboxylases
FILE REFERENCE: BB-1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,106
                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Microsoft Office 97
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NAME: Osman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59032/DJB/RAO
APPLICANT:
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TELEPHONE: (415) 494-8700
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LOCATION:
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es 19; Conservative (
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hes 19; Conserv
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                                                       Application US/09041075A
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Heidler, Steven A
Radding, Jeffrey A
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277..1365
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100.0%; Pred. No. 24;
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SEQ ID NO 4
LENGTH: 2000
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US-09-595-684B-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Heidler, Steven A
APPLICANT: Radding, Jeffrey A
TITLE OF INVENTION: IPC SYNTHASE GENES FROM FUNGI
FILE REFERENCE: X-11242 Sequence Let
Patent No. H002022
Patent No. H002022
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CURRENT FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/043,591
PRIOR FILING DATE: 1997-04-15
NUMBER OF SEQ ID NOS: 24
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SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/041,075A
CURRENT FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/043,591
PRIOR FILING DATE: 1997-04-15
PRIOR FILING DATE: 1997-04-15
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                              GENERAL
                                                                                                                                                                              Sequence 30, Application US/09595684B Patent No. 6544766
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NAME/KEY: CDS
LOCATION: (300)..(1739)
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ORGANISM: Candida kruisii
TITLE OF INVENTION: Human kinesins and methods of producing TITLE OF INVENTION: and purifying human kinesins FILE REFERENCE: cytop036 CURRENT APPLICATION NUMBER: US/09/595,684B
                                                                                                APPLICANT: Beraud, Christophe
APPLICANT: Ohashi, Cara
APPLICANT: Sakowicz, Roman
APPLICANT: VAisberg, Eugeni
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TYPE: RNA
ORGANISM: Candida kruisii
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nes 19; Conservative (
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                                                                                                                                                                    INFORMATION:
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                                                                Wood, Kenneth
Yu, Ming
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100.0%; Pred. No.
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Pred. No. 25;
5; Mismatches
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25;
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; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 09/295,612
; PRIOR FILING DATE: 2000-04-20
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 8257
; TYPE: DNA
; ORGANISM: Human
                                                                                                                                                                                                                                                                                      APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
NUMBER OF SEQ ID NOS: 1105
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US-09-620-312D-130
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                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (91)..(8082)
US-09-620-312D-130
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                                                                                                                                                                                                                                           SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 130
LENGTH: 8503
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Best Local Similarity
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                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                           FEATURE:
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2141 TTGATCTGGAGAAAGAATT 2159
                                2873 TTGATCTGGAGAAAGAATT 2891
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Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
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Wang, Jian-Rui
Zhou, Ping
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Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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                                                                   Conservative
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                                                                   Mismatches
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                                                                                   DB 4;
25;
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25;
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Search completed: April Job time: 165.43 secs

9, 2004, 08:20:42

RESULT 15 US-09-163-748C-3/c

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                                                                                                                                                             US-09-163-748C-3
                                                                      Query Match
Best Local Similarity
Matches 19; Conserv
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CURRENT FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09163748C Patent No. 6509172
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DeBacker, Oliver
APPLICANT: Van den Eynde, Benoit
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Encode Member
TITLE OF INVENTION: Family, The Proteins Encoded, And Uses Thereof
FILE REFERENCE: LUD 5558
                                                                                                                                                                              LENGTH: 9531
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: unsure
LOCATION: 92,232,1041,7412,9038-9040
OTHER INFORMATION: identity of several nucleotides not known
  7045 TACAAAATGAAAACAAAA 7027
                                    91 ТАСААЛАТGАЛААСЛАЛА 109
                                                                              Conservative
                                                                                               0.6%; Score 19;
100.0%; Pred. No.
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Maximum DB
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length: 2000000000
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13304.392 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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9888
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                16 US-10-257-166-123
14 US-10-311-455-124
15 US-10-311-455-482
14 US-10-311-455-482
14 US-10-311-455-482
12 US-10-311-455-4
12 US-10-01-843-87
13 US-10-01-843-87
14 US-10-36-734-1
14 US-10-36-734-1
15 US-10-074-475-133
16 US-10-074-475-133
17 US-10-282-1299-91177
18 US-10-282-1299-91176
19 US-10-424-599-91176
19 US-10-108-260A-1756
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Sequence 1, Appli
Sequence 1, Appli
Sequence 133, App
Sequence 91177, A
Sequence 91176, A
Sequence 91176, A
Sequence 1756, Ap
Sequence 1, Appli
                                                                                                                                                                                                                                                           Description
                                                                                                                                                             Sequence 123, App
Sequence 1214, Ap
Sequence 250839,
Sequence 482, App
Sequence 4, Appli
                                                                                                                               Sequence 170, App
Sequence 87, Appl
                                                                                                                                                                                                                                                                                                                                                           printed,
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16
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US-10-066-543-188	US-10-242-535A-1924	US-10-085-783A-192	US-10-312-841-	US-10-312-841-	US-10-271-416-	US-10-311-455-209	0-221-7	US-09-768-781-5	0-240-452-	US-10-240-485-90	-10-311-455-	-10-240-453	-10-311-455-	US-10-239-676-221	-10-221-714A-49	-10-311-455	US-10-257-166-17	-10-311-455	0-452-3	-10-311-455-	-10-311-455-	-10-311-455-1	21 - 714I	US-10-240-453-7	US-10-311-455-1828	-10-221-613-3	US-10-311-455-2123	US-10-311-455-796	US-10-221-714A-98
_	19246,	15	0		Sequence 8, Appli	2	e 5(5	equence 12,	e 90, A	e 1064,	e 323,	e 2217,	e 221,	æ	1793	17,	191,	e G	e 291,	e 208	e 188	e 353	e 7,	Sequence 1828, Ap	e 376	e 212	e 796	Sequence 98, Appl

ALIGNMENTS

RESULT 1

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US-10-257-166-123

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2000-09-01

NUMBER OF SEQ ID NOS: 178

SEQ ID NO 123

LENGTH: 6136

TYPE: DNA

ORGANISM: Artificial Sequence
                                                                                                                                                  ; FEATURE: ; OTHER INFORMATION: chemically treated genomic DNA US-10-257-166-123
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Publication No. US20040023230A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation
TITLE OF INVENTION: Genes Implicated in Pharmacogenomics
FILE REFERENCE: 5013.1011
CURRENT APPLICATION NUMBER: US/10/257,166
CURRENT FILING DATE: 2002-10-07
PRICA APPLICATION NUMBER: PCT/EP01/07470
                                                                        Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-06-29
                                                                                                                                                                                                                                                                                                                                                                DE 10032529.7
DE 10043826.1
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2122
                    3145 TATTTTGTTTTTTTTTGGTAAA 3166
TATTTTTTTTTTTGGTAAA 2143
                                0.7%;
__arity 100.0%;
Conservative ritingram
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                                                                                          Score 22; DB 16; Length 6136; Pred. No. 3.6;
                                                                          Mismatches
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RESULT 2

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US-10-311-455-1214
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION UNMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-027-632-250839
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US-10-027-632-250839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1214
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Publication No. US20030204075A9
Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern TITLE OF INVENTION: cytosine methylation FILE REFERENCE: 5013.1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, Christian APPLICANT: BERLIN, Kurt
                          Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2002-04-30 PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                          LENGTH: 21
TYPE: DNA
                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 325720
                                                                                                                                                                                                                                                          PRIOR FILING DATE:
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                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/146,002
APPLICATION NUMBER: US 60/146,002
FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
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  0.6%; Score 21; DB 15; ilarity 100.0%; Pred. No. 11; Conservative 0; Mismatches C
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; TYPE: DNA; ORGANISM: Artificial Sequence; PRATURE: PRATURE: OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens); OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens)
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US-10-311-455-482
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                                                                        , OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: OLEK, Al
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LENGTH: 6048
                                                                                                                                                                 NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 4
LENGTH: 6072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/10311455 publication No. US20030143606A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune TITLE OF INVENTION: cytosine methylation FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, Cl APPLICANT: BERLIN, Kurt
Matches
              Query Match
Best Local Similarity
                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                            APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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21; Conserv
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o. US20030143606A1
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  Conservative
                  0.6%; Score 21; DB 14; Length 6072; 100.0%; Pred. No. 12;
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00.0%; Pred. No.
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US-10-221-714A-170

3717 TATTTTGTTTTTTTTGGTAA 3737

TATTTTGTTTTTTTTGGTAA 3165

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US-10-001-843-87; Sequence 87, Application US/10001843; Publication No. US20020132255A1
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SEQ ID NO 170
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                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                   FILE REFERENCE: DEX-0267
CURRENT APPLICATION NUMBER: US/10/001,843
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/249,992
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 218
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PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
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FILE REFERENCE: 5013.1005
CURRENT APPLICATION NUMBER: US/10/221,714A
CURRENT FILING DATE: 2003-01-21
                                                                                                                                                       APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
APPLICANT: Turner, Leah
APPLICANT: Turner, Leah
APPLICANT: Turner, Leah
APPLICANT: Turner, Leah
APPLICANT: Turner, Leah
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PRIOR APPLICATION NUMBER: DE 10013847.0
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OFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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0; Mismatches
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Query Match

0.6%;

Score 20;

DB 14;

Length 654;

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GENERAL INFORMATION:

APPLICANT: ROMEO, Tony

TITLE OF INVENTION: SSCHERICHIA COLI CSRB GENE, RNA ENCODED

TITLE OF INVENTION: THEREBY, AND METHODS OF USE THEREOF

FILE REFERENCE: 316082002001

CURRENT APPLICATION NUMBER: US/09/736,734

CURRENT FILING DATE: 2000-12-13

PRIOR APPLICATION NUMBER: 09/112,584

PRIOR APPLICATION NUMBER: 60/052,372

PRIOR APPLICATION NUMBER: 60/052,372

PRIOR APPLICATION OMBER: 60/052,372

PRIOR PILING DATE: 1997-07-11

NUMBER OF SEQ ID NOS: 10
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SEQ ID NO 1
LENGTH: 654
TYPE: DNA
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: ROMEO, TONY
APPLICANT: ROMEO, TONY
TITLE OF INVENTION: ESCHERICHIA COLI CSRB
TITLE OF INVENTION: THEREBY, AND METHODS
FILE REFERENCE: 316082002001
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Best Local Similarity
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Patent No. US20020015983A1
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                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/396,911
CURRENT FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US/09/736,734
PRIOR FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 09/112,584
PRIOR FILING DATE: 1998-07-09
                                                                                                     PRIOR APPLICATION NUMBER: 60/052,372
PRIOR FILING DATE: 1997-07-11
NUMBER OF SEQ ID NOS: 10
                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Escherichia coli
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ORGANISM: Homo sapien
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100.0%; Pred. No.
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Pred. No.
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US-10-074-475-133
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Matches 20; Conserv
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                                                                                     ; OTHER INFORMATION: Clone ID: PAT_MRT3847_53343C.1 US-10-424-599-91177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 133, Publication No.
                                                                                                                                                                         APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
FILE REFERENCE: 38-21(53223)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 91177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local
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CURRENT FILING DATE: 2002-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific TITLE OF INVENTION: Genes and Proteins FILE REFERENCE: DEX-0313
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BQ ID NO 133

LENGTH: 1023
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                             Matches
                                                     Query Match
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APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                ORGANISM: Glycine max
                                                                                                                                                                 ENGTH: 1377
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                             Local Similarity
hes 20; Conserva
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1368 CAGTGGCATTGTCCAGCTTG 1387
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Cafferkey, Robert
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Conservative 0;
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ilarity 100.0%; Pred. No. 35;
Conservative 0; Mismatches
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                                                DB 12; Length 1377; 35;
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US-10-282-122A-10949/c
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FILE REFERENCE: ELITA, 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PEPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-25
PRIOR PEPLICATION NUMBER: 60/207,727
PRIOR PELING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.1
SEQ ID NO 10949
LENGTH: 1461
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APPLICANT: Zamudio, Carlo
APPLICANT: Malone, Cheryl
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blication No. US20040029129A1
                                                                                                                            Sequence 91176, Application US/10424599 Publication No. US20040031072A1
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PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Remaining Prior Application data removed - See File Wrapper or NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-02-16
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
                                                               APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/230,347 FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/267,636 FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/230,335 FILING DATE: 2000-09-06
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                                                                                                                                                                                                                                                           1073 ATATATGCTTTTAGTTTTGT 1054
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Zyskind, Judith
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Yamamoto, Robert
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APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560A1el full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PAtentin Ver. 2.1
SEQ ID NO 1756
LENGTH: 2418
TYPE: DNA
ORGANISM: Homo sapiens
US-10-108-260A-1756
                                                      CURRENT APPLICATION NUMBER: US/09/947,953
CURRENT FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: 60/230,311
PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: 60/295,889
PRIOR FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 2985
TYPE: DNA
TYPE: DNA
TORGANISM: Homo sapiens
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US-09-947-953-1/c
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US-10-108-260A-1756
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US-10-424-599-91176
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CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 91176
LENGTH: 1589
TYPE: non.
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Best Local :
Query Match
                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09947953
patent No. US20020155101A1
GENERAL INFORMATION:
APPLICANT: DONAHUE, J. KEVIN
APPLICANT: MARBAN, EDUDARDO
TITLE OF INVENTION: CARDIAC ARRHYTHMIA TREATMENT METHODS
FILE REFERENCE: 71699/56415
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ORGANISM: Glycine max
FEATURE:
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0.6%; Score 20; DB
Local Similarity 100.0%; Pred. No. 38;
hes 20; Conservative 0; Mismatches
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Local Similarity 100.0%; Pred. No. 36;
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0.6%; Score 20; DB 9;
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Pred. No.

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REFERENCE AUTHORS TITLE	KEYWORDS SOURCE ORGANISM	ACCESSION VERSION	RESULT 1 AX078761 LOCUS DEFINITION		O (1 C	4 4	C 40	c 38	37	ა თ თ	C 34	c 32		c 29		c 26	25 #	c 223	2 ×	20	c 19		16	14		o 0 11		വ ന ശ		თ ს	4.17	ωı	N L	No.	3	
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 1909)
Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M.
Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wong, C., Wu, H.C.,
Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y.,
Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M.,
Southwick, A., Tripp, M.G., Wu, T., Satou, M., Seki, M., Shinn, P.,
Ecker, J.R. and Theologis, A.
Arabidopsis Open Reading Frame (ORF) Clones
Unpublished
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Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Seker, J.R. and Theologis, A.
                                                                                                                                                                                                                                 The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada, K., Chan, M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Chen, H., Cheuk, R., Jones, T., Kim, C.J., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Davis, R.W.,
                                                                                                                                                                                                                                                                                                                                                                   Submitted (14-FBB-2003) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAPL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                      Yamada, K. (SSP/PGEC) and Seki, M. (R
to this work. Shinozaki, K. (RIKEN
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                                                                                                Annotation based on July 2002
                                                                                                                                                                                                                   Ecker, J.R. and Theologis, A.
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                                                          Location/Qualifiers
/mol_type="mRNA"
                      organism="Arabidopsis thaliana"
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                        CTTGCAAGTGATTATGACTCGGATGTGAGTCAAAAGAGCCATGGATCACGAAAGCAG
                                                                                                                  GTGGATAATGCTTCTGAGGAAGAGAATGATTCCGATGCTTTTGGATGATTCTGATGACGAC
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/db xref="G1:28393933"
/translation="MSSRAGEMSKEKNVQGGYRPEVEQLVQGLAGTRLASSQDDGGEW
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IQANISGRGRALSRKYDNNFVAPPVSRPPLEGGMNWQARGGSAQHTAVQBFPDVBDD
VDNASEEBUNDSDDDLASDDVDSVQOKHGRSKQNKWFKKKFTGSLDSLSIEQ
INEPQRQWHCPACQNOFGAIDWYNLHFULAHATKGARRVKLHRELAEVLEKDLQWRG
ASVLPCGEINGGWKGLGEDEKDYEIVWPPWVLIMWTRLDKDDNUKWLGMGNGELLEYF
DKYEALRARSYGPQGHRGMSVLMFESSATGYLEAEKLHRELAEWGLDRIAWGQDLWF
FSGGVRQLYGFLATKQDLDIFUNGHSGATTGYLEAEKLHRELAEMGLDRIAWGQDLWF
FKNKLSKQNKHAKVLEESLEIMSEKLRRTAEDNRIVRQRTKMQHEQNREEMDAHDRFF
MDSIKQIHBRRDAKEENFEMLQQDERAKVVGQQQQNINESNDOCRKRAEEVSSFIEF
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FEATURES

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Location/Qualifiers
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Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (contributed equally to this work as PIs.

d equally to (SSP/PGEC)

Annotation based on July 2002 version of the Arabidopsis genome

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1 (bases 1 to 2162)

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1 (yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Yu, G., Yuan, S., Carninci, P., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Shina, P., Suuthwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
Arabidopsis Full Length cDNA Clones
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Arabidopsis thaliana clone RAFL14-93-K05 (R20243) unknown protein
(At5g23570) mRNA, complete cds.
BT002944 BT002944.1 GI:27754622
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN carbidopsis Full-Length cDNA'); Seki,M., Narusaka,M., Ishida,J., Sabudu,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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mrna join (1963,10371328,14401684,17871953,2044>2254) /product="SGS3" cds join (1963,10371328,14401684,17871953,20442254) /codon_start=1 /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /product="SGS3" /pr	FUBMED 10850495 2 (bases 1 to 2254) AUTHORS Beclin,C., Mourrain,P., Vaucheret,H. and Elmayan,T. TITLE Direct Submission JOURNAL Submitted (28-FEB-2000) Biologie Cellulaire, INRA, Route de Saint-Cyr, Versailles 78026, France FEATURES 12254 /organism="Yrabidopsis thaliana" /mol type="genomic DNA" /cultivar="Columbia" /db xref="taxon:3702"	RESULT 4 AF239719 AF239719 AF239719 AF239719 DEFINITION ARABIdopsis thaliana SGS3 gene, complete cds. ACCESSION AF239719 VERSION AF239719.1 GI:8164029 KEYWORDS SOURCE ARABIdopsis thaliana (thale cress) ACGESSION AF239719.1 GI:8164029 KEYWORDS SOURCE ARABIDOPSIS THALIANA (thale cress) SPERMATOPHYTA; Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Brassicales; Brassicaceae; Arabidopsis. REFERENCE 1 (bases 1 to 254) MOURTAIN, P., Beclin, C., Elmayan, T., Feuerbach, F., Godon, C., Morel, J.B., Jouette, D., Lacombe, A.M., Nikto, S., Picault, N., Remoue, K., Sanial, M., Vo, T.A. and Vaucheret, H. TITLE posttranscriptional gene silencing and natural virus resistance JOURNAL 20306668	Qy 1561 GCAAAGGAGGAGATTTCGAGATGTTGCAGCAGCAGCAGGTTGTTGGCCAG 1620
QY 721 TATAACCTGCACCTCTACTAGCTGAGGAGAAAAGGACTAGGGAGTAAAGGACTAGGCAGTTAAGCTGCACCTCTACCTGCAGGCAAAAAGGACCTAGGCGAGTTAAGCTC 780 Db 721 TATAACCTGCACCCTCTACTAGCTCATGCAGACAAAAGGAGCTAGGCGAGTTAAGCTC 780 QY 781 CATAGAGAATTGGCTGAAGTTTTAGAAAAGGATCTACAGATGAGAGGCGCATCTGTCATT 840	CTTGCAAGTGATTGACTCGGATGTGAGTCAAAAGAGCCATGGATCACGAAAGCAG [Qy 241 AGAGGTAGCAACGTATCTTGGGAGAACAATGTATCCGGGAGAGGTAACGGCAATGGT 300	PKNKLSKQNKHAKVLEESLEIMSEKLARTAEDNRIVRORTKMQHEQNREEMDAHDRFF MDSIKQIHERRDAKEENFEMLOQQERAKVVGQQQQNINFSSNDDCRKRAEEVSSFIEF QEKEMEEFVEEREMLIKDQEKKMEDMKKRHHEEIFDLEKEFDEALEQLMYKHGLHNED D" ORIGIN Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 963; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 963; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 963; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Oy 1 ATGAGTTCTAGGGCTGGTTCAAGGATGTCTAAGGAACGTTCAGGGTGGTTATAGGCCT 60 Db 1 ATGAGTTCTAGGGCTTGGTTCAAGGTTGTAAGGAACGACTAGGTTGGTT

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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Submitted (02-APR-1999) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
On Sep 15, 2000 this sequence version replaced gi:4589439.
Address for correspondence: kos@@kazusa.or.jp For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd graph.cgi?c=MQMI Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/),
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Structural analysis of Arabidopsis thaliana chromosome 5. X.
Sequence features of the regions of 3,076,755 bp covered by sixty
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Arabidopsis thaliana genomic
AB025633 BA000015
AB025633.2 GI:10178221
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FEATURES
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similar to unknown protein"
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MDSIKQIHERNDAKKENFEMLGQQERAKVVGQQQQNINFSSNDDCRKAAEEVSSFTEF
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MDSIKQIHERDAKENFAMLTAGDCRKAMEDWKKRHHEBIFDLFDLAKEFDBALEQLMYKHGLHNED
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/translation="MATDSQPNQKLTLPLKTRIALTVISTMTDNAQREDGTINRRFLR
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NADLSRCFFAGDSAGGNIAHNVAIRICREPRSSFTAVKLIGLISIQPFFGGEERTEAE
NADLSRCFFAGDSAGGNIAHNVAIRICREPRSSFTAVKLIGLISIQPFFMVVVAGFDPL
KQLVGAPLVSPDRTDWCWKAMGLNRDHEAVNVGGPNAVDISGLDYPSTMVVVAGFDPL
KDWQRSYYEWLKLCGKKATLIEYPNWFHAFYIFPELPEAGQLIMRIKDFVDERVASLS
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VIVEGKNLIKKGIKGGPDHEGGIFTVEAPLHASNVQVVDPVTGRPCKVGVKYLEDGTK
VRVARGTGTSGSIIPRPEILKIRATPRPETTAGPKDTPMEFTVBGTYDAKTGKGMPDL"
join(16823. 16952,17143. 17320,17412. 17493,17675. 17851,
17943. 118110,18199. 118390)
/note="gene_id:MQM1.19"
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complement (join (18965. 19043,19240. 19298,19419.
19666. 19739,19908. 19961,20387. 20530))
/note="contains similarity to unknown protein emb|CAA22897.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="merlorifgagggighaspdsptldtseovyisslallmonkhg
Ragvpmevmgimlgbevdeytmrvudvfamfosgtgysveavuhvfgytmyldvikort
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Rapmvvgwyhshegfgcwlsgvdintgosfdallnehyysiainvrkobleekolle
Sindotimlogerottskrineottobmlslaakvnkavobedelspeklaivnvgr
Lhkkkwtdgltilrrfdthskrineottobmlslaakvnkavobedelspeklaivnvgr
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/product="50S_ribosomal_protein_L24"
/protein_id="BAA97247.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="gene_id:MQM1.20"
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/translation="MOKMONAIE
/translation="MOKMONAIE
/translation="MOKMONAIE
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TYMOREYGFAICLSACIFICTLLSMLYPFNRKLLTLLAIILEFTGLIMYSLSYIPFAR
TMYSKIFMTCFDTEF"
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/product="26S proteasome, non-ATPase regulatory subunit"
/protein_id="BAA97246.1"
/db_xref="GI:8809705"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oin(14922.
join(25614. .25838,26061. .26207,26324. .26438,26516. .2
26710. .26813,27522. .27765,27943. .28036,28115. .28305,
28385. .28604,28688. .28855,28944. .29092)
/note="gb|AAC97420.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similar to unknown protein"
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strong similarity to unknown protein"

1d:MQM1.16

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Query Match
Best Local S
Matches 963
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TATAACCTGCACCCTCTACTAGCTCATGCGAGGACAAAAGGAGCTAGGCGAGTTAAGCTC
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                                                                                                                   GAACCACAGAGGCAGTGGCATTGTCCAGCTTGTCAGAACGGACCTGGTGCCATCGATTGG
                                                                                                                                                         GAACCACAGAGGCAGTGGCATTGTCCAGCTTGTCAGAACGGACCTTGGTGCCATCGATTGG
                                                                                                                                                                                                                                                                 CTTGCAAGTGATGATTATGACTCGGATGTGAGTCAAAAGAGCCATGGATCACGAAAGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGGGGCATTCAAGCTAACATATCTGGTCGGGGACGAGCGTTGAGCAGAAAGTATGATAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAGGTAGCAACGTATCTGGGAGAGAGAAACAATGTATCCGGGAGAGGTAACGGCAATGGT
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//protein_id="BAA97243.l"
//db_xref="gi:809702"
//db_xref="gi
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30341. .30493,30579. .30722,30956. .31484))
/note="gene_id:MQM1.15
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AEKKLITEKEEEDKKTN"
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100.0%; Pr
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Query Match Best Local Similarity Matches 289; Conserv

12.7%; ilarity 99.7%; Conservative

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Score 239; DB 8; Pred. No. 9.9e-131; 0; Mismatches 1;

Length 650;

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Gaps

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ACCESSION
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                                                           misc_feature
                                                                                                                                                                                                                    source
                                                                                                                                                                                                                             Submitted (21-NOV-2002) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infoblogen.fr).
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brunaud, V., Balzergue, S., Dubreucg, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A.
T_DNA integration into the Arabidopsis genome depends on sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brunaud, V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                         /clone_lib="Arabidopsis thaliana
1. .650
                  /note="T-DNA
left border"
                                                                                                         /clone="157C08"
                                                                                                                                                /mol_type="genomic DNA"
/cultivar="Wassillewskija"
                                                                                                                             db_xref="taxon:3702"
                                                                                                                                                                                           organism="Arabidopsis thaliana'
                                      flanking sequence
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CEB (bases 1 to 18928)

RS Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alabrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alabrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alabrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alabrooks, S., Baden, H., Alapriano, D., Baden, H., Alabrooks, S., Barber, M., Barnstead, M., Benahmed, F., Balawin, D., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Biswalo, K., Blair, J., Barrell, K., Caderon, E., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Checkell, R., Cox, C., Coyle, M., Cree, A., D. Souza, L., Cleveland, C., Davis, R., Carden, R., Chen, Y., Chen, Z., Chu, J., Chelea, V., Chen, Z., Chu, J., Chelea, M., Cree, A., D. Souza, L., Cleveland, C., Davis, R., Carden, R., Chen, Y., Dublin, H., Divya, K., Daval, B., Eaves, K., Dayal, R., L., Chelea, R., Chen, Y., Dublin, H., Divya, K., Daval, B., Eaves, K., Dayal, R., Carden, M., Garcia, M., Foster, M., Foster, M., Foster, M., Foster, M., Foster, M., Gorrer, M., Gebregeorgis, B., Geer, K., Gill, R., Grady, M., Guerra, M., Gebregeorgis, B., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, M., Harrandez, C., M., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, M., Hernandez, J., Harvey, Y., Havlak, P., Hawes, A., Henderson, M., Hernandez, J., Jackson, A., Hollins, B., Howells, S., Hulyk, S., Khan, Z., King, L., Li, Z., Liu, J., Kowat, C., Liu, Y., London, P., Longacre, S., Johnson, R., Jolivet, A., Jackson, A., Hollins, B., Howells, S., Kally, S., Khan, Z., King, L., Li, Z., Liu, J., Liu, J., Liu, Y., London, P., Longacre, S., Loyez, J., Liu, J., Liu, J., Kovat, C., Liu, J., Kovat, C., Liu, J., Kovat, C., Liu, J., Kovat, J., Liu, J., Liu, J., Liu, J., Liu, J., Kovat, J.,
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HTG; HTGS PHASE1; HTGS DRAFT; HTGS ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Mammalia; Eutheria; Rodentia;
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Baylor Plaza, Houston, TX 77030, USA
On Oct 11, 2002 this sequence version replaced gi:21909375.
On Oct 11, 2002 this sequence version replaced gi:21909375.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas in the feature table contig scaffold). Within each contig-scaffold, assembly (a 'contig-scaffold'). Within each contig-scaffold, assembly (a 'contig-scaffold') within each contig-scaffold in the sequence by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
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Direct Submission
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3 (bases 1 to 178928)
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is is not known and their order in this sequence record as arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence This record will be updated with the accession number will be second as it is available and the accession number will
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Center clone name: CH230-32812
Center clone name: CH230-32812
Center clone name: CH230-32812
Center clone name: CH230-32812
Center clone name: Phrap; version 0.990329
Assembly program: Phrap; version 0.990329
Consensus quality: 149332 bases at least Q30
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Contact: hgsc-help@bcm.tmc.edu
Project Information
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176580
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/organism="Rattus norvegicus"
                                                                                                                         Location/Qualifiers

    Genome Center

                                                                                                                                                                               175436: contig of 175436 bp in length
175536: gap of unknown length
176579: contig of 1043 bp in length
176679: gap of unknown length
178928: contig of 2249 bp in length.
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REFERENCE
AUTHORS
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Mouse DNA sequence from clone RP23-419G21 on
During sequence assembly data is compared from overlapping clones.
                         Contact: humquery@sanger.ac.uk
                                         Web site:
                                                    Center: Wellcome Trust Sanger Institute Center code: SC
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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clone_end:T7
site:MboI
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clone_end:T7"
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173824. .175436
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clone_end:Sp6"
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clone_end:Sp6"
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/note="wgs_end_extension
lone_end:Sp6"
                                      http://www.sanger.ac.uk
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156410. .157915
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100.0%; Pred. No.
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Best Local Similarity
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: RMBL; Sw: SWISSPROT; TR:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep RP23-419G21 is from the RPCI-23 Mouse BAC Library constructed by the group of Pieter de Jong.
FOOT further details see http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 214186)

Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Dietrich, N.L., Eagle, W.O., Gupta, J., Ho, S.-L., Buffard, G.G., Dietrich, N.L., Eagle, W.O., Gupta, J., Ho, S.-L., Huang, M.C., Idol, J., Lee-Lin, S.-Q., Maduro, Q.L., Maduro, V.B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Ojodu, M.A., Pearson, R., Stantrippg, S., Summers, T.J., Thomas, J.W., Thomas, P.J., Stantrippg, S., Summers, T.J., Thomas, J.W., Thomas, P.J., Walker, M.A., Wetherby, K.D. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC078933 214186 bp DNA linear HTG 11-A Mus musculus chromosome 5 clone RP23-201E13 strain C57BL6/J, WORKING DRAFT SEQUENCE, 17 unordered pieces.
AC078933 AC078933 1 GI:9795569 HTG; HTGS_DRAFT.
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                                                                                                                                        Submitted (11-AUG-2000) NIH Intramural Sequencing Center, Grovemont Circle, Gaithersburg, MD 20877, USA
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                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                      Unpublished
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                                                                                                                                                                                                                                   Green, E.D.
                                                                                                                                                                                                                                                                                                                     NISC Mouse Sequencing Initiative
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                                                                                                                                                                                                                                                                 (bases 1 to 214186)
Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
                                                         Center: NIH Intramural Sequencing Center Center code: NISC
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="2"
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                                                                                                                      Genome Center
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Assembly program: Phrap; version 0.990319
Consensus quality: 207891 bases at least Q40
Consensus quality: 207891 bases at least Q30
Consensus quality: 207977 bases at least Q20
Consensus quality: 209797 bases at least Q20
Insert size: 118000; agarose-fp
Insert size: 218000; pulse-field-gel
Insert size: 217806; sum-of-contigs
Quality coverage: 4.43x in Q20 bases; agarose-fp
Quality coverage: 4.43x in Q20 bases; pulse-field-gel
Quality coverage: 4.94x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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153409
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135716
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/note="assembly_fragment"
                                                         3308. .7622
                                                                                                                                                                                           /mol_type="genomic DNA"
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                                                                                                                                                                                                                         organism="Mus musculus"
                                                                                                                                                                                                                                                                             87528 gap of unknown length
100606: contig of 13078 bp in length
100706: gap of unknown length
117904: contig of 17198 bp in length
118004: gap of unknown length
135715: contig of 17711 bp in length
135815: gap of unknown length
135816: gap of unknown length
135816: gap of unknown length
153408: contig of 17593 bp in length
153508: gap of unknown length
18134: contig of 27526 bp in length
181134: gap of unknown length
                                                                                                                                                     db_xref="taxon:10090"
chromosome="5"
                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                     note="assembly_fragment"
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                                                                                                                                                                                                                                                   . .214186
                                                                                                                                 lone="RP23-201E13"
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3307: gap of unknown length
7622: contig of 4315 bp in length
                           .13087
                                                                                                                     lib="RPCI
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ig of 5365
of unknown
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Best Local Similarity
Matches 22; Conserv
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Mus musculus chromosome 5 clone RP23-203F6 strain C57BL6/J, WORKING
DRAFT SEQUENCE, 16 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                   AC079182.1 GI:9886001
HTG; HTGS PHASE1; HTGS DRAFT.
Mus musculus (house mouse)
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                                                                               Direct Submission
Submitted (23-AUG-2000) NIH Intramural Sequencing
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 218774)
                                                                                                                                         Green, E.D.
                                                                                                                                                                                           NISC Mouse Sequencing Initiative
                                                                                                                                                                         Unpublished
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                           Center: NIH Intramural Sequencing Center Center code: NISC
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77446. .87428
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135816. .153408
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tive 0; Mismatches
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FEATURES

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NOTE: This is a 'working draft' sequence. It currently consists of 16 contigs. The true order of the pieces is not known and their order in this sequence record is
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Consensus quality: 208040 bases at least Q40
Consensus quality: 211445 bases at least Q30
Consensus quality: 213463 bases at least Q20
Insert size: 227000; gyarose-fp
Insert size: 242000; pulse-field-gel
Insert size: 217074; sum-of-contigs
Quality coverage: 4.40x in Q20 bases; sgarose-fp
Quality coverage: 4.91x in Q20 bases; sum-of-contigs
Quality coverage: 4.91x in Q20 bases; sum-of-contigs
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Center clone name: 203F06
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                                    /note="assembly_fragment"
4971. .8469
          /note="assembly_fragment"
                                                                                                           note="assembly_fragment"
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/chromosome="5"
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strain="C57BL6/J"
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218774: contig of 33829
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of 9488
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of 7299
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of 5663
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RS Muzny, D. Marie., Metsker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alabrooks, S., Amin, A., Anguiano, D., Barber, M., Baca, E., Baden, H., Badwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Benahmed, F., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., D. Gouza, L., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Durnha, D., Durbin, K., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Ferrandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Gebregoergis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gebregoergis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, W., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
Rattus norvegicus (Norway rat)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus clone CH230-11F1, WORKING DRAFT SEQUENCE,
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21732. .29661
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184946. .218774
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|53457. .184845
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Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Zoliver, A., Karpathy, S., Keily, S., Keily, S., Kaily, S., Kaily, S., Kaily, S., Kaily, S., Kaily, S., Kay, L., Li, Z., Liu, J., L
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NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC140364
Mus musculus chromosome UNK clone RP24-75K5, WORKING SEQUENCE, 8 unordered pieces.
AC140364
AC140364.2 GI:38176012
AC140364.2 GI:38176012
AC140364.7 BHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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                                                                                                                                                                                                                                                                                     2 (bases 1 to 280016)
McPherson, J.D. and Wat
Direct Submission
                                                                                                                                                                                                                                                                                                                                               wilson, R.K.
The sequence of Mus musculus clone
Unpublished
The Second Control of Musculus Clone
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 280016)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
Center: Washington University Genome (Center code: WIGSC Web site:http://genome.wustl.edu Contact: submissionn@watson.wustl.edu Contact: Project Information
                                                                                                                                      Direct Submission
Submitted (05-NOV-2003) Genome Sequencing Center, 4444 Forest Park
Submitted (05-NOV-2003) USA
Parkway, St. Louis, MO 63108, USA
On Nov 5, 2003 this sequence version replaced gi:28475622.
                                                                                                                                                                                                                                      Parkway, St. Louis, MO
3 (bases 1 to 280016)
                                                                                                                                                                                                                                                     Submitted (23-FEB-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                Wilson, R.K.
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235232. .236508
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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233371. .235181
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125418: gap of unknown length
180275: contig of 54857 bp in length
180375: gap of unknown length
236508: contig of 56133 bp in length.
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00.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                and Waterston, R.H
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                                                                                                      Genome Center ------
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Sciurognathi; Muridae; Murinae; Mus
                                                                                       Genome Sequencing Center
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2.1;
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RESULT 14
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AC073813 304407 bp DNA linear HTG 29-JUN-200 Mus musculus clone RP23-69B1, WORKING DRAFT SEQUENCE, 58 unordered
                                                                                                                                                                                     22;
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                                                                                                           TGTGAGTCAAAAGAGCCATGGA 58654
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/note="assembly_name:Contig28"
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/note="assembly_name:Contig26"
127786. .198220
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48534. .85803
/note="assembly_name:Contig25"
oson/
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98321. .280016
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/db_xref="taxon:10090"
/chromosome="UNK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="RP24-75K5"
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1302: gap of unknown length
3866: contig of 2564 bp in length
3966: gap of unknown length
24768: contig of 20802 bp in length
48433: contig of 20802 bp in length
48433: contig of 33565 bp in length
48533: gap of unknown length
48533: gap of unknown length
85903: gap of unknown length
127685: contig of 37270 bp in length
127685: contig of 41782 bp in length
198220: contig of 70435 bp in length
198220: contig of 70435 bp in length
198320: gap of unknown length
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100.0%; Pr
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Pred. No. 2.1;
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unknown length
of 23565 bp in length
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VERSION
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TITLE
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AC073813
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Consensus quality: 257140 bases at least Q40
Consensus quality: 282847 bases at least Q30
Consensus quality: 288639 bases at least Q30
Consensus quality: 288639 bases at least Q20
Estimated insert size: 272860; agarose-fp estimation
Estimated insert size: 298707; sum-of-contigs estimation
Quality coverage: 9.46 in Q20 bases; agarose-fp estimation
Quality coverage: 8.64 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 58 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
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Center clone name: RPCI-23_69B1
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Center: Joint Genome Institute
Center Code: JGI
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DOE Joint Genome Institute.
Sequencing of Mouse
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Mus musculus (house mouse)
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Direct Submission
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Mammalia; Eutheria; Rodentia;
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1267: gap of unknown length
2281: contig of 1014 bp in length
2381: gap of unknown length
gap of unknown
contig of 1850
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contig of 1436
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contig of 1260
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t unknown
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of 1397
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37829 40231 40331 42295 42395

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157121:
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171481:
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3: gap of unknown length
2: contig of 7779 bp in length
1: contig of 14249 bp in length
1: contig of 14249 bp in length
1: gap of unknown length
1: contig of 7480 bp in length
1: contig of 6680 bp in length
1: contig of 6680 bp in length
1: gap of unknown length
1: gap of unknown length
1: gap of unknown length
2: contig of 12477 bp in length
3: contig of 8284 bp in length
2: contig of 800 bp in length
2: contig of 10528 bp in length
3: contig of 10528 bp in length
4: contig of 10528 bp in length
5: gap of unknown length
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6: gap of unknown length
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Ng, W. V., Kennedy, S.P., Mahairas, G.G., Berquist, B., Pan, M., Shukla, H.D., Lasky, S.R., Baliga, N., Thorsson, V., Sbrogna, J., Shukla, H.D., Lasky, S.R., Baliga, N., Thorsson, V., Sbrogna, J., Swartzell, S., Weir, D., Hall, J., Dahl, T.A., Welti, R., Goo, Y.A., Leithauser, B., Keller, K., Cruz, R., Danson, M.J., Hough, D.W., Leithauser, B., Keller, K., Cruz, R., Danson, M.J., Hough, D.W., Dale, H., Maddocks, D.G., Jablonnik, P.E., Krebs, M.P., Angevinne, C.M., Dale, H., Isenbarger, T.A., Peck, R.F., Pohlschrod, M., Spudich, J.L., Jung, K.-H., Alam, M., Freitas, T., Hou, S., Daniels, C.J., Dennis, P.P., Jung, K.-H., Alam, M., Freitas, T., Hou, S., Daniels, C.J., Hood, L. and Omer, A.D., Ebhardt, H., Lowe, T.M., Liang, P., Riley, M., Hood, L. and
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Abb15067 Drosophil
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SGS3 gene; post-transcriptional inactivation; RNA degradation; viral resistance; resistance; fatty acid content; protein content;

88.

Nucleotide sequence of the Arabidopsis SGS3 polypeptide.

15-MAY-2001 AAF25374;

(first

entry)

AAF25374 standard; cDNA; 1878

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26-JAN-2000; 2000FR-00001006.
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The present sequence encodes the Arabidopsis thaliana SGS3 polypeptide The SGS3 gene is essential for post-transcriptional inactivation (degradation of RNA) and for resistance to viruses. Overexpression of

Claim 1; Page 32-35; 36pp; French.

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                                                                                                                                                                     The present sequence represents the genomic sequence of the Arabidopsis thaliana SGS3 gene. The SGS3 gene is essential for post-transcriptional inactivation (degradation of RNA) and for resistance to viruses. Overexpression of SGS3 results in plants with increased resistance to viruses, while inactivation of SGS3 in transgenic plants (e.g. by expressing antisense RNA, by mutation or by homologous recombination) increases the level of the transgene product. This product may e.g. impart resistance (to herbicide, insects or pathogens), alter contents of essential fatty acids or proteins, or is pharmaceutically active, e.g. & essential fatty acids or proteins, or is pharmaceutically active, e.g.
                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 31-32; 36pp; French.
                                                                                                                                                                                                                                                                                                                                                                                           New SGS3 gene from Arabidopsis thaliana, useful for increasing virus resistance in plants and, when inhibited, for increasing transgene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                    pCR primers AAF25371-72 were used to amplify cDNA encoding an Arabidopsis thaliana SGS3 polypeptide. The SGS3 gene is essential for post-transcriptional inactivation (degradation of RNA) and for resistance to viruses. Overexpression of SGS3 results in plants with increased resistance to viruses, while inactivation of SGS3 in transgenic plants (e.g. by expressing antisense RNA, by mutation or by homologous (e.g. impart resistance (to herbicide, insects or pathogens), alter may e.g. impart resistance (to herbicide, insects or pathogens), alter contents of essential fatty acids or proteins, or is pharmaceutically active, e.g. an immunoglobulin or interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JUL-2000; 2000WO-FR002052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200105951-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AVET )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUL-1999; 99FR-00009417.
26-JAN-2000; 2000FR-00001006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 22; 36pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-159529/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beclin C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New SGS3 gene
resistance in
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27
                                                                                                                                                                                                                                         AAF25371 standard; DNA; 23 BP
                                                                                                            SGS3 gene; post-transcriptional inactivation; viral resistance; resistance; fatty acid conte
                                                                                                                                                                                    15-MAY-2001
                                                                                                                                                                                                               AAF25371;
                                                                                                                                                       PCR primer
                                          WO200105951-A2
                                                                    Arabidopsis thaliana
             25-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer;
                                                                                                                                                                                                                                                                                                                                           1855 GGCCTTCACAATGAAGATGATTGA 1878
                                                                                                primer;
                                                                                                                                                                                                                                                                                                                    27
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INST NAT RECH AGRONOMIC
                                                                                                                                                                                                                                                                                                                                                                        l Similarity
24; Conserv
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                                                                                                                                                                                                                                                                                                                   GGCCTTCACAATGAAGATGATTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88
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                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 6 A;
                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                    88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from Arabidopsis thaliana, useful for increasing virus plants and, when inhibited, for increasing transgene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA encoding an Arabidopsis SGS3 polypeptide.
                                                                                                                                                                                     (first entry)
                                                                                                                                                        cDNA encoding an Arabidopsis SGS3 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                         1.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  7 C; 5 G; 9 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGRONOMIQUE.
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                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                          Score 24;
                                                                                                                                                                                                                                                                                                                                                                                             Pred.
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0.71;
                                                                                                                       content;
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                                                                                                                                    RNA
                                                                                                                                                                                                                                                                                                                                                                                                             Length 27;
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                                                                                                                        protein
                                                                                                                             content;
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RESULT 5
AAF12773
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Best Local S
Matches 20
 PCR primers AAF25371-72 were used to amplify cDNA encoding an Arabidopsis thaliana SGS3 polypeptide. The SGS3 gene is essential for post-transcriptional inactivation (degradation of RNA) and for resistance to viruses. Overexpression of SGS3 results in plants with increased viruses. While inactivation of SGS3 in transgenic plants resistance to viruses, while inactivation of SGS3 in transgenic plants (e.g. by expressing antisense RNA, by mutation or by homologous (e.g. impart resistance (to herbicide, insects or pathogens), alter may e.g. impart resistance (to herbicide, insects or pathogens), alter contents of essential fatty acids or proteins, or is pharmaceutically active, e.g. an immunoglobulin or interferon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AVET )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JUL-1999; 99FR-00009417.
26-JAN-2000; 2000FR-00001006.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beclin C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 22; 36pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New SGS3 gene from Arabidopsis resistance in plants and, when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-159529/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23
                                                                                                                                                                                                                    Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; expressed sequence trag; Fusarium venenatum; Aspergillus niger; Aspergillus oryvae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
                                                                                                                                                                                                                                                                                                                                                                               AAF12773 standard; cDNA; 596 BP
                                                                                                                                                                                                                                                                                                  Aspergillus oryzae EST SEQ ID NO:5296.
                                                                                                                                                                                                                                                                                                                              13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                       AAF12773;
                                                                                                              22-MAR-2000; 2000WO-US007781
                                                                                                                                           28-SEP-2000
                                                                                                                                                                    WO200056762-A2.
                                                                                                                                                                                               Aspergillus
                                                                                         22-MAR-1999;
WPI; 2000-594572/56
                         Berka RM,
                                                (NOVO ) NOVO NORDISK BIOTECH INC (NOVO ) NOVO NORDISK AS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVENTIS CROPSCIENCE SA.
INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arcacirciaccicicicic 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGAGTTCTAGGGCTGGTCC 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Elmayan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 6 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                          Rey MW,
                                                                                                                                                                                               oryzae.
                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99FR-00009417
                                                                                          99US-00273623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 C; 7 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                              Shuster JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaucheret H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s thaliana, ι
n inhibited,
                                Kauppinen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for increasing virus
, for increasing transgene
                                 s,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                    Clausen IG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                       Olsen PB;
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CC cells. The method uses fluorescence-labeled nucleic acids isciacular CC the FF cells and a substrate of expressed sequence tags (RST). The ESTs CC are used in the methods for monitoring differential expression of genes CC in a first filamentous fungal (FF) cell relative to expression of the CC same genes in one or more second filamentous fungal cells. Monitoring the CC global expression of genes from FF cells allows the production potential CC of the microorganisms to be improved. New genes may be discovered, CC possible functions of unknown open reading frames can be identified and CC gene copy number variation and stability can be monitored. The expression CC of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, CC metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of credundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF11248 to AAF11247 represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents CC Aspergillus orgzae; and AAF14879 to AAF1337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present
RESULT 6
AAH93017/c
ID AAH93017 standard;
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Best Local S
Matches 20
               Daly M,
                                                                                                                                                                                                                                    WO200142511-A2
                                                                                                                                                                                                                                                                                                           chromosome
                                                                                                                                                                                                                                                                                                                                             Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;
                                                                                                                                                                                                                                                                                                                                                                               Human inflammatory bowel disease related gene fragment
                                                                                                                                                                                                                                                                                                                                                                                                                      09-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH93017;
                                                                                                      10-DEC-1999;
10-APR-2000;
                                                                                                                                                          11-DEC-2000; 2000WO-US033632
                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                              single nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monitoring differential expression of genes in filamentous fungal cells uses fluorescence-labeled nucleic acids isolated from the cells and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         substrate of expressed sequence tags.
                                                   ELLI-)
                                                                    (WHED )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        431 TCCAAGAAGAACAAGAACAA 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 TCCAAGAAGAACAAGAACAA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88; Page 2210; 3161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sion of genes in a first filamentous fungal (FF) cell relative sion of the same genes in one or more second filamentous fungal The method uses fluorescence-labeled nucleic acids isolated from the method uses fluorescence
                                                                    WHITEHEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                 WHITEHEAD INST BIOMEDICAL RES. ELLIPSIS BIOTHERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                           5q31-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention describes a method for monitoring differential of genes in a first filamentous fungal (FF) cell relative
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                                                                                                     99US-0170257P.
2000US-0196046P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 144 A; 168 C; 150 G; 134 T;
                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                            polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                       forensic test; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>,</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 20;
Pred. No.
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                                                                                                                                                                                                                                                                                                                          chromosome 19p13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 596;
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                                                                                                                                                                                                                                                                                                                        paternity test;
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검

Lander ES,

Rioux J,

Siminovitch

sequences and their corresponding proteins AAA81304 to AAA81321 represent PCR primers

the

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AAA81465/c
ID AAA814
XX
AC AAA814
AC AAA814
XX
DT 04-DEC
XX
N. men.
XX
Neisse
KW Neisse
KW Mening
XX
Neisse
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Neisse
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PR 09-OCT
PR 30-APR
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PF 108-OCT
PR 30-APR
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ISOLAT
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Matches 20
                                                                                                                                                                                                                       Frazer CM, ... Galec.
             The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81180 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81259 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a method for detecting the presence of polymorphisms associated with inflammatory bowel diseases such as ulcerative colitis and Crohn's disease. The methods can be used to detect the presence of genetic polymorphisms associated with inflammatory bowel disease and correlating their occurrence with disease states. They may be used in this way for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis. The present sequence is a gene containing a polymorphic site described in the exemplification of the
                                                                                                         Claim 7; Page 383-397; 1760pp; English.
                                                                                                                                        Neisserial infections,
                                                                                                                                                       Isolated nucleotide sequences of Neisseria meningitidis which in the diagnosis and treatment of N. meningitidis infection an
                                                                                                                                                                                                      WPI; 2000-318079/27.
                                                                                                                                                                                                                                                                                                                                  09-OCT-1998;
30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                08-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Meningococcus B; MenB; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis; Neisseria gonorrheae; genome; antigen; vaccine; diagnosis; infection; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N. meningitidis partial DNA sequence gnm_13 SEQ ID NO:13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Testing for the presence of polymorphisms associated with inflammatory bowel disease, using a hybridization assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-367874/38.
                                                                                                                                                                                                                                                                                                  (CHIR ) CHIRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1696 TTTCAAGAGAAAGAGATGGA 1715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415 TTTCAAGAGAAGAGATGGA 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          700
                                                                                                                                                                                                                                                    Hickey E,
V, Galeotti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.1%;
llarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                 98US-0103794P
99US-0132068P
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                                                                                                                                       for example, N.gonorrhoea.
                                                                                                                                                                                                                                                                    Peterson
                                                                                                                                                                                                                                                      Mora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 58 
Mismatches
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Ratti G,
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58;
                                                                                                                                                                                                                                                    H, Venter
Scarselli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          identification;
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                                                                                                                                                                                                                                                    Scarlato
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                                                                                                                                                                       can be used
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ABQ88198/c
ID ABQ881
XX ABQ881
XX ABQ881
XX IB-SEP
XX Human
XX Human;
KW Osteor
XX Osteor
XX Homo (
XX PN WO200;
XX PD 27-JU
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AAA81489 5/c
AAA81489 5/c
Continuation (6 of 9) of AAA81489 from base 500001 (N. mening
Continuation (6 of 9) of Fragments LOCUS AAA81489 Accession
WP Sequence split into 9 fragments LOCUS AAA81489 Accession
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 47475 BP; 11600 A; 13758 C; 12290 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            variable regions
                                                                                                                                                             Human; osteoblast; stem cell differentiation; bone tissue deposition.
                                                                                                                                                                                                                                                                                                                               ABQ88198 standard; cDNA; 154902
                                                                                                                                                                                                                                                  18-SEP-2002
                                                                                                                                              osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fragment Name
AAA81489 0
AAA81489 1
AAA81489 2
AAA81489 2
AAA81489 3
AAA81489 4
AAA81489 5
AAA81489 6
AAA81489 6
                                                               WO200250301-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 GAACAGTTGGTTCAAGGTTT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                         osteoblast differentiation related cDNA SEQ ID NO 105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                osteopathic; ss.
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27-JUN-2002

RASSULT 10
AAF21612/c
ID AAF216
XX AAF216
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XX OS-NOV
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PR 30-APR
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Neisseria meningitidis

diagnosis; antigen; detection; infection;

08-MAR-2000; 2000WO-US005928.

09-NOV-2000 WO200066791-A1

30-APR-1999; 08-OCT-1999;

99US-0132068P. 99WO-US023573.

Neisseria meningitidis B nucleotide sequence SEQ ID NO:113

Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine;

gene therapy; antibacterial;

AAF21612 standard;

DNA;

0

13-MAR-2001

(first

entry)

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XFXRRXGRXGRXFFFXXXXSSSSSSSSSSSSSSSSSXXX
                                                                                                                                                                                  The invention relates to genes and their expression profiles are used for: (a) screening modulators of precursor stem cell differentiation into conteoblasts, or bone tissue deposition; (b) diagnosing abnormal constepoprosis; or (c) treating or monitoring treatment of the conditions conteoblast formation or cited in (b), or monitoring the progression of bone tissue deposition, cited in (b), or monitoring the progression of bone tissue deposition. CC specific conditions include postmenopausal osteoporosis, glucocorticoid constepoprosis or male osteoporosis, osteopenia, osteopory, drugtinduced abnormalities in bone formation or bone loss, conditions that consider abnormalities in bone formation or bone loss, conditions that consider abnormalities in bone formation or bone loss, conditions that consider abnormalities of the printle osteoporosis). CC involve altered bone metabolism (e.g. idiopathic juvenile osteoporosis). CC sequence date for this patent did not form part of an osteoblast confideration associated CDNA marker of the invention. Note: The confideration, but was obtained in electronic format directly from WIPO cat first the printled sequences as the printled confideration, but was obtained in electronic format directly from WIPO at first properties.
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Best Local S
Matches 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-DEC-2000;
24-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-2001; 2001WO-US048276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ji D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 105; 78pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-557663/59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            process.
                                                                                                                                                         Sequence 154902 BP; 43917 A; 31458 C;
128153
                                     1712 TGGAGGAGTTTGTGGAAGAG 1731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Axelrod DW,
                                                                                 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENE LOGIC INC.
PROCTER & GAMBLE CO.
                                                                                                    Similarity
TGGAGGAGTTTGTGGAAGAG 128134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0255882P.
2001US-0285691P.
                                                                               Conservative
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                                                                                                    1.1%; Score 20;
100.0%; Pred. No.
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                                                                                      Mismatches
                                                                                                                                                                 32848 G; 46679 T; 0 U; 0 Other;
                                                                                                           DB 6;
54;
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                                                                                          0; Indels
                                                                                                                            Length 154902;
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RESULT 11
AAA68016/c
ID AAA680
XX AAA680
XX AAA680
XX Eucaly
XX Plant;
KW Pinus
XX Pinus
XX WO2000
XX Eucaly
XX O9-OCT
PF 06-OCT
XX O9-OCT
PR 14-JUI
XX
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                         09-OCT-1998;
14-JUL-1999;
                                                                                                                                                                                                                                                               Plant; lignin; lignin bi
Pinus radiata; Monterey
                                                                                                                                                                                                                                                                                                                                  Eucalyptus grandis CCR nucleotide sequence SEQ ID NO:109.
                                                                                                                                                                                                                                                                                                                                                                                                                         AAA68016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA68016 standard; DNA; 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the outer membrane proteins currently used
                                                                                         06-OCT-1999;
                                                                                                                                                                              WO200022099-A1
                                                                                                                                                                                                                      Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                24-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 349980 BP; 86473 A; 95646 C; 85908 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis B full length
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Rappuoli R, Frazer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2000; 2000GB-00004695
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAACAGTTGGTTCAAGGTTT 167805
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V, Galeotti C, Mora |
R, Frazer CM, Grandi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                         98US-00169789
99US-0143811P
                                                                                                                                                                                                                                                                                 lignin biosynthetic pathway; Eucalyptus grandis;
                                                                                       99WO-NZ000168
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100.0%; Pr
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Pred. No.
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, Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genome sequence and open reading prevent Neisserial infections.
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Scarselli M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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The present invention describes isolated polynucleotides and proteins cencoding and representing the enzymes cinnamate 4-hydroxylase (C4H), CC commarate 3-hydroxylase (C3H), phenolase (PNL), O-methyl transferase (C0M), cinnamyl alcohol dehydrogenase (CND), Cinnamyl acohol dehydrogenase (CND), cinnamyl-COA reductase (CCC), phenylalanine ammonia-lyase (PAL), 4-coumarate:COA ligase (4CL), CC coniferol glucosyl transferase (CGT), coniferin beta-glucosidase (CBG), CC cacid methyl transferase, caffeoyl COA methyl transferase, caffeic cacid methyl transferase, caffeoyl COA methyl transferase, coumerate COA (CC ligase, cytochrome p450 LXX1A, diphenol oxidase, flavanol glucosyl cransferase, flavanol hydroxylase, and isoflavone reductase, which are convolved in the lignin biosynthetic pathway. The polynucleotides can be composed to modulating lignin content, lignin composition and the structure cof a plant, especially eucalyptus and pine species, and for modifying the cactivity of an enzyme involved in lignin biosynthetic pathway, and for corpoducing a plant having altered lignin content, composition and content. The lignin content can be efficiently modified using the colynucleotides. AAA67908 to AAA68201 and AAB16341 to AAB16449 represent composition of the polynucleotide and protein sequences used in the exemplification of the corposition and protein sequences used in the exemplification of the corposition of the corposition and protein sequences used in the exemplification of the corposition.
    Matches
                             Query Match
Best Local :
                                                                                                Sequence 481 BP; 122 A; 118 C; 111 G; 130 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel polyncleotide encoding enzymes involved in lignin-biosynthetic pathway useful for producing transgenic plants especially eucalyptus and pine species having altered lignin content, composition and structure.
                                                                                                                                                 present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 91-92; 213pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-317962/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENESIS RES & DEV CORP LTD.
       19;
                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ĕ
  Conservative 0;
                                                 1.0%;
                        Score 19;
Pred. No.
         Mismatches
1.8e+02;
0;
                                                   DB 3;
                                                 Length 481;
       Indels
    0,
    Gaps
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ADD41766/c
ID ADD417
XX
AC ADD417
XX
DT 15-JAN
XX
Cinnam
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XX
Lignin
XX
Lignin
XX
US2003
XX
PN US2003
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PN US2003
XX
PN 10-JUL
XX
PF 18-JUN
PF 18-JUN
PR 21-NOV
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                                        11-SEP-1996;
21-NOV-1997;
09-OCT-1998;
14-JUL-1999;
12-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                  10-JUL-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biosynthesis;
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                                                 2000US-00615192
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                                                                                          98US-00169789
99US-0143833P
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97US-00975316.
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ARK64246
ID AAK64
XX AAK64
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DT O6-N
XX Human
XX Human
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Best Local S
Matches 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated polynucleotide. The polynucleotides, polypeptides and genetic constructs are useful for modulating lignin content, composition and structure of plants, or for producing a plant having altered lignin content, composition and structure. The polynucleotides are also useful in genome mapping, physical mapping, positional cloning of genes, or as non-disruptive tags for marking organisms, particularly plants. The present sequence represents a polynucleotide associated with the lignin biosynthetic pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotide associated with the lignin biosynthetic pathway, for modulating lignin content, composition and structure of plants, or producing a plant with altered lignin content, composition and structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-829606/77.
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    07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
                                                                                                                                                                                                           16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
                                                                                                                                                                                                                                                                                                                     31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:9306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAK64246 standard; cDNA; 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK64246;
                                                                                                                                                                     28-JUN-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                            17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BLOKSBERG L N.
HAVUKKALA I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
  ; 2000US-0179065P.

2000US-0184664P.

2000US-0184664P.

2000US-0186350P.

2000US-0199076P.

2000US-0199076P.

2000US-0199123P.

2000US-029467P.

2000US-0214866P.

2000US-021648P.

2000US-0216647P.

2000US-0216489P.

2000US-0216489P.

2000US-021649P.

2000US-021649P.

2000US-0218690P.

2000US-0218690P.

2000US-021869P.

2000US-0220966P.

2000US-0220966P.

2000US-0220966P.

2000US-0220966P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry) .
                                                                                                                                                                                                                                                                                                                                                                                                                               2001WO-US001354.
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Pred. No.
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1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                 14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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22-AUG-2000;
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23-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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25-SEP-2000;

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27-SEP-2000;

29-SEP-2000;

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14-SEP-2000;
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14-SEP-2000;
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14-AUG-2000;
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12-SEP-2000;
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2000US-0225213P.

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08-DEC-2000;
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                                                                                                                                                                 Ruben SM;
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human immune/hematopoietic diagnosing and/or treating cancers polypeptides, and metastasis.

Claim 1; SEQ ID NO 9306; 3071pp + Sequence Listing; English.

CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) CC amino acid sequences given in AAW82170 to AAW91921. (I) have cytostatic cactivity, and can be used in gene therapy and vaccine production. (I) CC proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to CC supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to prevent the secreted (I), by inserting the CC nucleic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK4703 CC to AAK87694 represent human immune/haematopoietic antigen genomic the present invention. AAK54942 to antigen genomic AAK54950 and AAM82169

Query Match Best Local Similarity

100.0%; 1.0%;

Score 19; Pred. No.

DB 2; L

Length 495

Sequence 495

BP; 126 A; 121 C; 116 G; 132 T; 0 U; 0 Other;

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RESULT 14
AAV23847/c
ID AAV238
XX AAV238
XX AAV238
XX Lignin
XX Lignin
XX Lignin
XX Lignin
XX Eucaly
PN W09811
XX HO9811
XX HO
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                                                                                                                      This sequence represents a fragment of the CCR enzyme coding sequence. It CC is an example of a DNA sequence of the invention, which are from CR Eucalyptus grandis (eucalyptus) and Pinus radiata (pine) associated with the lignin biosynthesis pathway. Constructs containing the DNA sequences can be used to produce transgenic plants or plant cells, especially woody plants e.g. eucalyptus or pine species but also e.g. monocotyledons or CC plants e.g. eucalyptus or pine species but also e.g. monocotyledons or CC dicotyledons; by stably incorporating the constructs into the plant CC genome. The lignin content or structure, or activity of a specific enzyme in the plant, can therefore be modulated. Reductions in lignin content or CC changes in composition are useful in tree processing for paper. High lignin content results in energy- and chemical-intensive separation methods in order to obtain the pure cellulose fibre required. Reductions in lignin content may also be useful for forage crops, whilst increases CC in lignin composition may be desirable to increase the mechanical strength of wood, change its colour or increase its resistance to rot.

The sequences are also useful as probes to isolate DNA sequences encoding
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences useful for modification of plant lignin content or structure from Eucalyptus grandis (eucalyptus) and Pinus radiata (pine) are associated with lignin biosynthesis pathway, useful e.g. in paper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 39; 82pp; English
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RESULT 15
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                                                                                                                                                            This sequence represents a cinnamoyl-CoA reductase (CCR) partial cDNA CC from Eucalyptus grandis. This enzyme is involved in the biosynthesis of CC lignin, an insoluble polymer which is primarily responsible for the CC rigidity of plant stems. Lignin serves as a matrix around the CC polysaccharide components of some plant cell walls. The higher the lignin CC content, the more rigid the plant. Lignin also plays a role in disease CC resistance of plants by impeding the penetration and propagation of CC pathogenic agents. Lignin is formed by polymerisation of at least three CC pathogenic agents. Lignin is formed by polymerisation of at least three CC pathogenic agents compared three monolignols are synthesised by similar CC sinapyl alcohol. These three monolignols are synthesised by similar CC pathways from phenylalanine in a multistep process and are believed to be CC plants can be altered using DNA sequences encoding these enzymes. CC Lignin content can be increased by incorporation of additional copies of genes encoding these enzymes into the target plant. This could be beneficial for increasing the mechanical strength of wood. Similarly, a decrease in lignin content can be obtained by transforming the target plant with antisense copies of such genes. This may be beneficial in CCC plants used as forage crops for livestock (lignin is indigestible) and in trees used in paper manufacture
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Best Local S
Matches 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grierson AW, Bloksberg LN, Havukkala I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lignin; biosynthesis; forage crop; wood; paper production; transgenic plant; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated DNA sequence encoding enzymes from the lignin synthetic pathway useful for generating plants with an altered lignin content.
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                                                                                                                                 Sequence 495 BP; 126 A; 121 C; 116 G; 132 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Col 37-38; 48pp; English.
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                             74 TGGTTCAAGGTTTGGCAGG 92
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                                                                                   Similarity
TGGTTCAAGGTTTGGCAGG 466
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ALIGNMENTS

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	JOURNAL COMMENT	TITLE	REFERENCE AUTHORS		SOURCE ORGANISM	ACCESSION VERSION KEYWORDS	RESULT 1 AQ959658/c LOCUS DEFINITION
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: at@tigr.org For addtional information, see http://www.tigr.org/tdb/at/at.html	polymorphisms Unpublished (2000) Contact: Xiaoying Lin	Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M. Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based	<pre>1 (bases 1 to 693) Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T.,</pre>	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	Arabidopsis thaliana (thale cress) Arabidopsis thaliana	A0959658 1 GI:6787359 GSS.	AQ959658 693 bp DNA linear GSS 28-JAN-2000 LEREM21TFB LERE Arabidopsis thaliana genomic clone LEREM21, genomic

Result No.

Score

Query Match Length DB ID Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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AQ959658 AQ959657 AV566465 AU236368

AQ959658 LEREM21TF AQ959657 LEREM21TF AV566465 AV566465 AU236368 AU236368

Description

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Class: shot
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/note="Organ: Leaf; Vector: pUC19JK; Total genomic sheared to 0.6-0.8 Kbp before ligation."
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/mol_type="genomic DNA"
/strain="LANDSBERG ERECTA"
/db xref="taxon:3702"
/clone="LEREM21"
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Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utter
Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C.,
Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M.
Genomic survey sequencing of Landsberg erecta ecotype of
Arabidopsis thaliana and identification of sequence-based
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: at@tigr.org
For addtional information, see
Seg primer: TF
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Unpublished (2000)
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/note="Organ: Leaf; Vec
sheared to 0.6-0.8 Kbp
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mol_type="genomic DNA"

/strain="LANDSBERG ERECTA"

/db xref="taxon:3702"

/clone="LEREM21"
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Kbp before ligation."
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Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.

A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries DNA Res. 7 (3), 175-180 (2000)

20363093
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                      ATGGAGGAGTTTGTGGAAGAGAGGGGGAGATGCTGATAAAAGATCAAGAGAAGAAGAAGATGGAA
                                                                   GACGATTGCCGAAAGAGCTGAGGAAGTGTCAAGCTTCATCGAGTTTCAAGAGAAAGAG
                                                                                      GACGATTGCCGAAAGAGAGCTGAGGAAGTGTCAAGCTTTCATCGAGTTTCAAGAGAAAGAG
                                                                                                                                  CAGCAGGAACGTGCCAAGGTTGTTGGCCAGCAGCAGCAGAACATTAATCCCTCTAGCAAT
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     ATGGAGGAGTTTGTGGAAGAGAGGGAGATGCTGATAAAAGATCAAGAGAAGAAGATGGAA
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asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol
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|mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998).cDNA cleaved with BamHI
and Khol was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
AU236368
AU236368.1 GI:19875537
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3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074,
Tel: 81-298-36-4359
Fax: 81-298-36-9060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Large scale analysis of Arabidopsis full-length cDNA Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
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AU236368 RAFL14 Arabidopsis 1
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AGAGGTAGCAACGTATCTGGGAGAGGAAACAATGTATCCGGGAGAGGGTAACGGCAATGGT
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                                                                                      AAAACTTGGGTTTCTCAGAATTCGAATCCTCCTAGAGCTTGGGGTGGTCAGCAAGGA
                                                                                                                                    GGAGGAGAGTGGGAGGTCATTTCCAAGAAGAACAAGAACAAACCAGGAAACACTTCTGGA
                                                                                                                                                                                                                                                                                                                                            ATGAGTTCTAGGGCTGGTCCAATGTCTAAGGAAAAGAACGTTCAGGGTGGTTATAGGCCT
                                              <u>AAAACTTGGGTTTCTCAGAATTCGAATCCTCCTAGAGCTTGGGGGTGGTCAGCAGCAAGGG</u>
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/tissue_type="root"
/lab_host="DH10B"
/clone_lib="RAFL14"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Tosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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LERGX20TF LERG Arabidopsis thaliana
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Unpublished (2000)
Contact: Xiaoying Lin
The Institute for Genomic Research
The Institute for Genomic Rockville,
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Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
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For addtional information,
Seq primer: TF
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Tel: 301 838 0200
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                           GAGGTTGAACAGTTGGTTCAAGGTTTGGCAGGACGAGACTGGCTTCTCTCACAAGATGAT
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301 838 0208
                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                   /clone_lib="LERG"
/note="Organ: Leaf; Vector: pUC19JK; Total genomic
/note="Organ: Leaf; Vector: pUC19JK; Total genomic
sheared to 0.4-0.7 Kbp before ligation."
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Arabidopsis thaliana"
/mol_type="genomic_DNA"
/strain="LANDSBERG_ERECTA"
/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                          clone="LERGX20"
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Pred. No. 4.5e-230;
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Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: of 12,028 non-redundant expressed sequence tags from norr size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)
20363093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGAGGTAGCAACGTATCTGGGAGAGAGAAACAATGTATCCGGGAGAGGGTAACGGCAATGGT
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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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       Conservative
                                                                                                                                                                /tissue_type="aboveground organs"
/dev_stage="two to six-week old"
/clone lib="Arabidopsis thaliana aboveground organs two to
six-week old"
                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="Columbia"
                                                                                                                                                                                                                                                           /db_xref="taxon:3702"
/clone="APD25d02R"
                                                                                                                                                                                                                                                                                                                                                    organism="Arabidopsis"
                                                                                                                                       note="Vector: pBluescriptII SK-;
                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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         Score 329; DB 9;
pred. No. 4e-156;
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457 bp DNA linear GSS 28-JUN-19:
Arabidopsis thaliana genome survey sequence T7 end of BAC F8G21 of
IGF library from strain Columbia of Arabidopsis thaliana, genomic
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/strain="Columbia"
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Contact: Xiaoying Lin
Contact: Xiaoying Lin
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, M
9713 Medical Center Dr., Rockville, M
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1 (bases 1 to 523)

1 (bases 1, Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utterbach, T., Feldblyum, T., Liang, F., Creasy, T. and Fraser, C.M.

Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based
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                                                                                                                                                                    GAAACACTTCTGGAAAAACTTGGGTTTCTCAGAATTCGAATCCTCCTAGAGCTTGGGGTG
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   GTAACGGCAATGGTCGGGGCATTCAAGCTAACATATCTGGTCGGGGACGAGCGTTGAGCA
                                   GTAACGGCAATGGTCGGGGCATTCAAGCTAACATATCTGGTCGGGGACGAGCGTTGAGCA 346
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/strain="LANDSBERG ERECTA"
/db_xref="taxon:3702"
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Pred. No. 1.8e-127;
0; Mismatches 3;
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Best Local Similarity
Matches 244; Conserv
                                                                                                                                                                                                                                                                                                      source
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    1635 TAATCCCTCTAGCAATGACGATTGCCGAAAGAGAGCTGAGGAAGTGTCAAGCTTCATCGA 1694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y., and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
AU227277
                                                                                                                                                                                                                                                                                                                                                          Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998).cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2002)
Contact: Motoaki Seki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Large scale analysis of Arabidopsis full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AU227277.1 GI:19741924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 81-298-36-9060
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                                               Conservative
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                                                                                                                                                                              /clone="RAFL14-93-K05"
/tissue_type="root"
/lab host="DH10B"
                                                                                                                                                                                                                                            /organism="Arabidopsis
/mol_type="mRNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                            /clone_lib="RAFL14"
/note="Site_1: BamHI; Site_2: SalI"
                                                                                                                                                                                                                                                                                                        .421
                                                                13.0%; Score 244; DB 9;
100.0%; Pred. No. 1e-112;
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                                                 Mismatches
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1022 GAGCACGCCATTCCTATGGTCCACAGGGCCATCGTGGGATGAGTGTTCTGATGTTTGAGA 1081
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F27C8TRC IGF Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other_GSSs: F27C8TFC
Contact: Steve Rounsley
Contact: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 290)
Rounsley, S.D., Suh, E.J., Wible, C., Golden, K., Shatsman, S., Choi, P., Yu, K., Akinretoye, B., Shen, K., Goonasekaram, S., Militscher, J., Adams, M.D. and Venter, J.C.
A BAC End Sequence Database for Indate Minimal Overlaps in A BAC End Sequence Database in Indate.
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AQ010650.1 GI:3165927
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis Genomic Sequencing. Update 4
                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: M13 Reverse
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                          Email: rounsley@tigr.org
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                                 adrigieric gecare gea acca a galacer geregea aractrice a ca a granda gerer tra
                                                                                                   Conservative
                                                                                                                                                                                    /sex="hermaphrodite"
/clone llb="IGF"
/note="Vector: BeloBACII; Site_1: EcoRI; Site_2:
Produced by Thomas Altmann"
                                                                                                                                                                                                                                                                                    /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia"
                                                                                                                                                                                                                                                      /db_xref="taxon:3702"
/clone="F27C8"
                                                                                                                                                                                                                                                                                                                                           .290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (1998)
                                                                                                                   12.1%;
                                                                                                    0; Mismatches
                                                                                                                    Score 228; DB 28; Pred. No. 1.3e-104;
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                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                      Matches 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                    1710 GATGGAGGAGTTTGTGGAAGAGAGGGGAGATGCTGATAAAAGATCAAGAGAAGAAGAATGGA 1769
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1142 TAGATAGAATTGCCTGGGGTCAGAAGCGCAGTATGTTTTCTGGAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ,123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Gorgo, S., Burns, D., Griffin, J., Konanoutoua, M., Muyen, D., Tan, R., Rose, M., Warren, B., Ton, B., Kastury, K., Borillo, C., Carpio, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, L., Turner, C., Krikorian, S., Elder, L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI999551
701556368 A. thaliana, Columbia Col-0, rosette-3 Arabidopsis thaliana cDNA clone 701556368, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pharmaceuticals, Inc.
4633 World Parkway Circle, St.
Tel: 877-577-2733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana
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AI999551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana Gene Expression MicroArray
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: service@genomesystems.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Systems, Inc., a wholly owned subsidiary of Incyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: David Smoller,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAGTGCCACTGGCTATTTGGAGGCCGAACGCCTCCACCGGGAGTTAGCTGAGATGGGGT
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                                                                                                                    Conservative
                                                                                                                                                                                                                /tissue_type="rosette"
/dev_stage="4 - 7 weeks"
/clome_lib="A. thaliana, Columbia Col-0, rosette-3"
/clome_lib="N. thaliana, Columbia Col-0, site_2: Sall; cDNA
/note="Vector: pSPORT; Site_1: NotI; Site_2: Sall; cDNA
library was derived from unTreated rosette tissue from
Arabidopsis thaliana, Columbia Col-0, at 4 - 7 weeks.

Plants were grown in 1:1:1 peat moss/vermiculite/perlite
soil at 22 deg. C +/- 3 deg. C under constant light, and
watered with fertilizer. cDNA synthesis was initiated
using a NotI-oligo(dT) primer. Double-stranded cDNA was
blunted, ligated to Sall adaptors, digested with NotI,
size-selected, and cloned into the NotI and Sall sites of
the pSPORT vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/cultivar="Columbia Col-0"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="701556368"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Arabidopsis thaliana"
                                                                                                                                                            9.0%;
                                                                                                                                         Score 169; DB 9;
; Pred. No. 2.2e-74;
                                                                                                                      0; Mismatches
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BH169457
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AUTHORS
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                                                                                 121
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Matches 153;
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                 110 CACAAGATGATGGAGGAGAGTGGGAGGTCATTTCCAAGAAGAACAAGAACAAACCAGGAA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 858 558 6379
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A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is single pass sequence recovered
                                                  ACACTTCTGGAAAAACTTGGGTTTCTCAGAATT
                                                                                                                                                                                                                                                                              GTTATAGGCCTGAGGTTGAACAGTTGGTTCAAGGTTTGGCAGGGACGAGACTGGCTTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="SALK_001394"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana lines
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"
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/strain="Columbia 0"
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                                                                                                                                                                                                                                                                                                                             Score 153; DB 20,
Pred. No. 2.3e-66;
153
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VERSION
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BH169448
                                                                           VERSION
KEYWORDS
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ORGANISM
                                                                                                                     ACCESSION
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                          407
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Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Pax: 858 558 6379
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Unpublished (2001)
Contact: Joseph R. Ecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated intron of At5g23570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ecker@salk.edu
                                                                                                                     BH169448 482 bp DNA linear GSS 03-OCT-200 SALK 001377 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_001377, genomic survey sequence. BH169448
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                                              GCAGTGCCACTGGCTATTTGGAGGCCGA 260
                                                                                                                                                                                                                                                                                                     GCAGTGCCACTGGCTATTTGGAGGCCGA 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="SAIK_039005"
/clone=lib="Arabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana lines
/note="PCR was performed on Arabidopsis thaliana lines
/note="PCR was performed one or more TDNA insertion
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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/db xref="tark"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 148; DB 28;
Pred. No. 1.1e-63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 443;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Salk Institute Genomic Analysis Laboratory
The Salk Institute for Biological Studies
1,0010 N. Torrey Pines Road, La Jolla, CA 92
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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1 (bases 1 to 482)
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AQ964581.1 GI:6792282
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; spermatophyta; Magnoliophyta; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                          Unpublished (2000)
                                                Seq primer: TR
Class: shotgun
                                                                                                                                                                                                                                                 polymorphisms
                                                                                        Email: at@tigr.org
For addtional information,
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/clone=lib="Arabidopsis thaliana TDNA insertion lines"
/clone=lib="Arabidopsis thaliana lines
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
the site of insertion.at line was
be found at http://signal.salk.edu/tdna_protocols.html"
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/mol_type="genomic DNA'
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source /0.232 / Organism="Arabidopsis thaliana" / mol_type="genomic DNA" / strain="LANDSBERG ERECTA" / strain="LANDSBERG ERECTA" / db xref="taxon:3702" / clone="LERGX20" / clone="LERGX20" / clone="LERGX20" / clone="LERGX20" / clone="LERGX20" / clone="Organ: Leaf; Vector: pUC19JK; Total genomic DNA was sheared to 0.4-0.7 Kbp before ligation." / conservative 0.4-0.7 Kbp before ligation." / conservative 0; mismatches 0; Indels 0; Gaps 0; Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0; / conservative 0; Mismatches 0; Indels 0; Gaps 0; / conservative 0; Mismatches 0; Indels 0; Gaps 0; / matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0; / matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0; / matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0; / matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0; / matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0; / matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0; / matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0; / matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0; / matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0; / matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0; / matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0; / matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0; / matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0; / matches 0; Indels 0; / matches 0; Indels 0; / matche
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Sequence 27, Appl
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		Sequence 1061, Ap Sequence 4961, Ap Sequence 2355, Ap	Sequence 36, Appl Sequence 594, App	Sequence 3, Appil Sequence 1728, Ap Sequence 940, App			Sequence 5, Appli Sequence 767, App Sequence 1214, Ap

; TYPE: DNA ; ORGANISM: Eucalyptus US-09-615-192A-109 CURRENT APPLICATION NUMBER: US/09/615,192A CURRENT FILING DATE: 2000-07-12 PRIOR APPLICATION NUMBER: US 08/975,316 PRIOR FILING DATE: 1997-11-21 PRIOR APPLICATION NUMBER: US 08/713,000 PRIOR RILING DATE: 1996-09-11 PRIOR FILING DATE: 1996-09-11 PRIOR FILING DATE: 1998-10-09 PRIOR FILING DATE: 1998-10-09 PRIOR FILING DATE: 1998-10-09 PRIOR FILING DATE: 1998-10-09 US-09-615-192A-109/c SOFTWARE: Fa SEQ ID NO 109 LENGTH: 481 GENERAL INFORMATION: APPLICANT: Bloksberg, APPLICANT: Havukkala, Sequence 109, Application US/09615192A Patent No., 6410718 Query Match Best Local Matches TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin FILE REFERENCE: 470 TEGTTCAAGGTTTGGCAGG 452 74 TGGTTCAAGGTTTGGCAGG 92 l Similarity 19; Conserv FastSEQ for Windows Version Bloksberg, Conservative 11000.1003c4U grandis 1.0%; Ilkka Leonard N. 0, Score 19; DB; Pred. No. 12; 0; Mismatches Lignin Content 4 Length 481 Indels ٥,

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US-09-169-789-109/c

Sequence 109, Application US/09169789 Patent No. 6653528 GENERAL INFORMATION:

APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilka
IIILE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003c2
CURRENT APPLICATION NUMBER: US/09/169,789
CURRENT FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 08/975,316
EARLIER FILING DATE: 1997-11-21
EARLIER FILING DATE: 1997-11-21

EARLIER APPLICATION NUMBER: US 08/713,000

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ORGANISM: Eucalyptus grandis
US-09-169-789-109
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NUMBER OF SEQ ID NOS: 185
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 109
LENGTH: 481
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOCTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/713,000
PILING DATE: September 11, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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les 19; Conserv
                                                                                                                                                                                                                                                                                               NAME: SLEATH, Janet 37,007 REGISTRATION NUMBER: 37,007 REFERENCE/DOCKET NUMBER: 11
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TYPE: nucleic acid
STRANDEDNESS: single
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2601 Elliott Avenue, Suite 4185
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100.0%; Pred. No.
                                                                  1.0%; Score 19; DB
100.0%; Pred. No. 12
tive 0; Mismatches
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RESULT 4

RESULT 6 US-09-041-075A-4

Application US/09041075A

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; Sequence 4, Applicati ; Patent No. H002022 ; GENERAL INFORMATION: ; APPLICANT: Heidler,

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CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
CURRENT FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR FILING DATE: 1996-09-11
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
PRIOR FILING DATE: 1998-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 495
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-615-192A-27
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                                                                                                                                            ; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-169-789-27
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                                                                                     Query Match
Best Local S
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APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods
TITLE OF INVENTION: Modification of Plant
                                                                                                                                                                                                                      SOFTWARE: F
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                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/169,789
CURRENT FILING DATE: 1998-10-09
EARLIER APPLICATION NUMBER: US 08/975,316
EARLIER FILING DATE: 1997-11-21
EARLIER APPLICATION NUMBER: US 08/713,000
EARLIER FILING DATE: 1996-09-11
NUMBER OF SEQ ID NOS: 185
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tent No. 6410718
                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bloksberg, Leonard N. APPLICANT: Havukkala, Ilkka
                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 185
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                    ENGTH: 495
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es 19; Conservative
                                                                       Local Similarity 100.
nes 19; Conservative
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484 TGGTTCAAGGTTTGGCAGG 466
                                   74
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                                   TGGTTCAAGGTTTGGCAGG 92
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APPLICANT: Radding TITLE OF INVENTION: FILE REFERENCE: X-Patent No. H002022

Radding, Jeffrey A
VENTION: IPC SYNTHASE GENES FROM FUNGI
NCE: X-11242 Sequence Lst

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; Sequence 30, Application US/09595684B
Patent No. 6544766
GENERAL INFORMATION:
APPLICANT: Beraud, Christophe
APPLICANT: Ohashi, Cara
APPLICANT: Ohashi, Cara
APPLICANT: Vaisberg, Roman
APPLICANT: Vaisberg, Eugeni
APPLICANT: Wood, Kenneth
                                                                                                                                                                                                                               RESULT 8
US-09-595-684B-30
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LENGTH: 2000
TYPE: RNA
ORGANISM: Candida kruisii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. H002022

CURRENT APPLICATION NUMBER: US/09/041,075A

CURRENT FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/043,591

PRIOR FILING DATE: 1997-04-15

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
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Best Local
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APPLICANT: Radding, Jeffrey A
APPLICANT: RADDING: IPC SYNTHASE GENES FROM FUNGI
TITLE OF INVENTION: IPC SYNTHASE GENES FROM FUNGI
TITLE PREFERENCE: X-11242 Sequence Let
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CURRENT FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/043,591
PRIOR FILING DATE: 1997-04-15
RUMBER OF SEQ ID NOS: 24
APPLICANT: Yu, Ming
TITLE OF INVENTION: Human kinesins and methods of producing
TITLE OF INVENTION: and purifying human kinesins
FILE REFERENCE: cytop036
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NAME/KEY: CDS
LOCATION: (300)..(1739)
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ORGANISM: Candida kruisii
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Pred. No. 12;
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APPLICANT: Zhou, Ping
APPLICANT: Ma, Yunqing
APPLICANT: Ma, Yunqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
ITILE OF INVENTION: No. 6569662el Nucleic Acids and
ITILE OF INVENTION: Polypeptides
FILE REFERENCE: 784C1P2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LENGTH: 8257
; TYPE: DNA
; ORGANISM: Human
US-09-595-684B-30
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                                S
                                                                                                                                     ; NAME/KEY: CDS
; LOCATION: (91)..(8082)
US-09-620-312D-130
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                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 1105
SOPTWARE: pt_FL_genes Version 1.0
SEQ ID NO 130
LENGTH: 8503
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 130, Application US/09620312D Patent No. 6569662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/595,684B
CURRENT FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 09/295,612
PRIOR FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
                                                                     Matches
                                                                                   Query Match
Best Local Similarity
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Best Local
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                                1802 TTGATCTGGAGAAAGAATT 1820
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2141 TTGATCTGGAGAAGAATT 2159
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19; Conserv
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Zhao, Qing A.
Wehrman, Tom
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Zhang, Jie
Ren, Feiyan
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                                                                     Conservative
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100.0%; Pred. No.
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                                                                     Mismatches
                                                                                       DB 4;
13;
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US-08-916-421B-1
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TITLE OF INVENTION:
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TYPE: DNA
ORGANISM: Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc feature
LOCATION: (28222)...(28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (84812)...
OTHER INFORMATION: n equals
NAME/KEY: misc feature
rocation: (98120)..(98120)
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OTHER INFORMATION: n
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OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals
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LOCATION: (191989)..(191989)
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UCATION: (309398). (309398)
OTHER INFORMATION: n equals NAME/KEY: misc feature OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (234814)...(234814) LOCATION: (309418)..(309418) OTHER INFORMATION: n equals LOCATION: (312837)..(312837) oTHER INFORMATION: n equals a, LOCATION: (312993) .. (312993) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (559241)..(559241) OTHER INFORMATION: n equals OTHER INFORMATION: n equals NAME/KEY: misc LOCATION: (319226)..(319226) OTHER INFORMATION: n equals NAME/KEY: misc_ NAME/KEY: misc NAME/KEY: misc_feature LOCATION: (657203). (657203) OTHER INFORMATION: n equals : NAME/KEY: misc_feature NAME/KEY: misc_feature 1074435). (674435) NAME/KEY: misc_feature LOCATION: (657081)..(657081) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (622708)..(622708) OTHER INFORMATION: n equals NAME/KEY: misc featu LOCATION: (600992).. OTHER INFORMATION: n equals LOCATION: (682442)...(682442) OTHER INFORMATION: n equals NAME/KEY: misc feature LOCATION: (713652)...(713652) OTHER INFORMATION: n equals LOCATION: (674435)...(674435)
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NAME/KEY: misc feature NAME/KEY: misc feature LOCATION: (741684)...(741684) OTHER INFORMATION: n equals LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (779676)...(779676) OTHER_INFORMATION: n equals OTHER INFORMATION: n equals NAME/KEY: misc LOCATION: (7794 NAME/KEY: misc_feature LOCATION: (871619)...(871619) OTHER INFORMATION: n equals NAME/KEY: misc_featu LOCATION: (855539).. NAME/KEY: misc_feature LOCATION: (1119881)..(1119881) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (1096846)...(1096846) OTHER INFORMATION: n equals a, NAME/KEY: misc_ LOCATION: (1084 NAME/KEY: misc_feature LOCATION: (1130881)..(1130881) OTHER INFORMATION: n equals INFORMATION: n equals (682442) . . (682442) (1084830)..(1084830) DRMATION: n equals a, feature feature feature feature feature feature equals (559167) (600992) (559241)(779455)a, a, a a a a a a a ρ a, a a a a a a, a a a, a a ŗ ŗ ŗ Ĺ ŗ , ŗ ή ŗ Ç ŗ ŗ ŗ ŗ Ç ŗ ŗ ŗ ú ç ņ ņ 'n Ç 'n ç ú 0 ņ ç ç ú 'n ç ç Ç ç ç õ ņ O Ç ဝူ ç or g S R õ õ õ 얹 ဝူ ဝူ o R õ or S ဝူ or ö 유 õ or Pr õ 유 õ õ ç a ω ø g g ω g g Ø ω ω

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                                                                                                                                                                                                                                                                                                        Sequence 5315, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
                                                                                                                                             NUMBER OF SEQ ID NOS:
SEQ ID NO 5315
LENGTH: 462
TYPE: DNA
                                                          Matches
                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                APPLICANT: GATY Breton et. al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709:2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR FILING DATE: 1999-01-29
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LOCATION: (1664854)..(1664855)
OTHER INFORMATION: n equals a,
                                                                                                                              ORGANISM: Klebsiella pneumoniae
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LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a,
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LOCATION: (1569020)..(1569020)
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LOCATION: (1470091)..(1470091)
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                                                                      Local Similarity
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Pred. No.
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RESULT 12 US-09-322-478-25/c ; Sequence 25, Application US/09322478

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EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 25
LENGTH: 1254
TYPE: DNA
ORGANISM: Pisum sativum
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Best Local Similarity
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                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 27805/3019
REFERENCE/DOCKET NUMBER: 27805/3019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
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APPLICANT: Voytas, Daniel F.
APPLICANT: Voytas, Daniel F.
TITLE OF INVENTION: Plant Retroelements and Methods Related Thereto
FILE REFERENCE: P-1065 ISURF Plant Retroelement
CURRENT APPLICATION NUMBER: US/09/322,478
CURRENT FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 05/087125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1829 base pair
                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wigler, Michael H. APPLICANT: Colicelli, John J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Inc
                                                                                                                                                                                                                                                                                                                         FILING DATE: 19
CLASSIFICATION:
STRANDEDNESS:
TOPOLOGY: li
                                 TYPE: NUCLEIC ACID
                                                                                                           TELEPHONE: (312)
TELEPHONE: (312)
TELEPHONE: (312)
TELEPHONE: (312)
                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
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                                                 1829 base pairs
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100.0%; Pred. No.
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FEATURE:

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US-07-688-352C-15
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US-08-474-379C-15
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Best Local Similarity
                           Best Local Similarity
Matches 18; Conserv
                                                            Query Match
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                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/206
FILING DATE: 01-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/688
FILING DATE: 19-APR-1991
ATTORNEY_AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 2786
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                     TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                           FEATURE:
                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07-JUN
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/01 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Illinois
COUNTRY: United States of America
                                                                                                            NAME/KEY:
LOCATION:
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   139 ATTTCCAAGAAGAACAAG 156
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                                                                                                                                                                                                       nucleic acid
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    Marshall, O'Toole, Gerstein, Murray & Borun
    South Wacker Drive/6300 Sears Tower

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Colicelli, John J.
VENTION: CLONIUS BY COMPLEMENTATION AND RELATED
VENTION: PROCESSES
                                                                                                                                                                                                                         1829 base pairs
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ilarity 100.0%;
Conservative (
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                       linear
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                                                                                                                                                                                         single
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100.0%; Pred. No.
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                                  Score 18; DB; Pred. No. 40; Mismatches
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Search completed: April Job time: 96.5698 secs

9, 2004, 08:20:46

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US-09-146-249A-15
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; LOCATION:
US-09-146-249A-15
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GENERAL INFORMATION:
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                                                                         Query Match
Best Local Similarity
                                                           Matches
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511
PILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                          TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wigler, Mi
APPLICANT: Colicelli,
TITLE OF INVENTION: C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1829 base pair
                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 6300 :
CITY: Chicago
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                              LENGTH: 1829 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                              139 АТТТССААGАAGAACAAG 156
 985 ATTTCCAAGAAGAACAAG 1002
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                                                                                                                                                                                                                                                                                                          312-474-0448
                                                              Conservative
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li, John J.

Cloning by Complementation and Related
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                                                                              100.0%;
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                                                                              Score 18; pred. No.
                                                                 Mismatches
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Perfect score:
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length: 2000000000
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/2/pubpna/US09A PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09B PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09B PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09 NEW PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10A PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10 PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10 NEW PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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397
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                                                                                                                                                                                                                                                                                               DB
   US-10-9-833-790-167
2 US-10-424-599-18549
5 US-10-027-632-2355
5 US-10-027-632-2355
5 US-10-027-632-11812
5 US-10-027-632-11812
5 US-10-027-632-11812
                                                                                                                             US-10-424-599-91177
US-10-424-599-91176
US-10-085-783A-19246
US-10-242-535A-19246
US-10-424-599-57837
US-10-174-693-293476
US-10-174-693-27
US-10-174-693-27
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Sequence 91177, A
Sequence 19176, A
Sequence 19246, A
Sequence 19246, A
Sequence 27937, A
Sequence 293476,
Sequence 203, App
Sequence 27, Appl
Sequence 167, App
Sequence 18849, A
Sequence 23556, A
Sequence 11811, A
Sequence 11812, A
Sequence 11812, A
Sequence 24736, A
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US-09-960-352-3954	US-09-960-352-12961	US-09-728-445-290	US-10-424-599-112786	US-09-960-352-14374	US-10-424-599-116017	US-09-960-352-12756	US-09-864-761-32008	US-10-029-386-26108	US-10-027-632-174763	US-10-419-723-1	US-10-067-514-1	US-10-085-117-145	US-10-117-722-130	US-10-037-270-130	US-10-071-766-51	US-10-133-013-260	US-09-893-519A-140	US-09-770-107-1	US-10-176-847-9	US-10-108-260A-1451	US-09-742-581-6	US-09-742-581-4	US-09-742-580-6	US-09-742-580-4	US-09-742-582-6	US-09-742-582-4	US-10-424-599-4367	US-09-938-842A-2465	US-09-938-842A-2465
		Sequence 290, App	Sequence 112786,	Sequence 14374, A	Sequence 116017,	Sequence 12756, A	Sequence 32008, A	Sequence 26108, A	17	Sequence 1, Appli	Sequence 1, Appli	Sequence 145, App	Sequence 130, App	130	Sequence 51, Appl	260	14(Sequence 1, Appli	9	149		4	σ,	e 4,	Sequence 6, Appli	4	4367,	Sequence 2465, Ap	Sequence 2465, Ap

ALIGNMENTS

US-10-424-599-91177
; Sequence 91177, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:

US-10-424-599-91176, Application US/10424599; Sequence 91176, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION: 밁 S ; OTHER INFORMATION: Clone ID: PAT_MRT3847_53343C. US-10-424-599-91177 NUMBER OF SEQ ID NOS: 285684 SEQ ID NO 91177 LENGTH: 1377 Matches Query Match Best Local (APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28 APPLICANT: La Rosa Thomas J ORGANISM: Glycine max FEATURE: TYPE: DNA 359 CAGIGGCATIGICCAGCTIG 673 CAGIGGCATIGTCCAGCTIG 692 20; Similarity Conservative 1.1%; °, Score 20; DB 12; Length 1377; Pred. No. 14; Mismatches 0, 0 Gaps 0

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SEQ ID NO 91176
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-10-424-599-91176
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PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
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CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
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                                     APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relatiing
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
CURRENT FILING DATE: 2002-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
                                                                                                                           APPLICANT: ChondroGene Inc. APPLICANT: Liew, C.C.
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PRIOR APPLICATION NUMBER: US 10/085,783 PRIOR FILING DATE: 2002-02-28
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ORGANISM: Human
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Zhou Yihua
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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification Single Nucleotide
TITLE OF INVENTION INVEST: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT EPILICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 57837
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Best Local &
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Best Local :
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PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
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APPLICANT: Kovalic David K
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ORGANISM: Human
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; Pred. No.
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RESULT 8
US-10-174-693-27/c
; Sequence 27, Application US/10174693
; Publication No. US20030131373A1
; GENERAL INFORMATION:
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SEQ ID NO 109
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 293476
LENGTH: 429
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Best Local Similarity
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APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods for the
TITLE OF INVENTION: Modification of Plant Lignin Content
FILE REFERENCE: 11000.1003C5
CURRENT APPLICATION UNDERS: US/10/174,693
CURRENT FILING DATE: 2002-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
PRIOR APPLICATION NUMBER: US 09/169,789
PRIOR FILING DATE: 1998-10-09
PRIOR APPLICATION NUMBER: US 09/615,192
PRIOR FILING DATE: 2000-07-12
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PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/174,693
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 08/975,316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin FILE REFERENCE: 11000.1003c5
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APPLICANT: Havukkala, Ilkka
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mes 19; Conserv
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100.0%; Pr/
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100.0%; Pred. No.
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Pred. No.
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47;
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US-10-424-599-18549/c
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; ORGANISM: Eucalyptus grandis
US-10-174-693-27
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         Sequence 18549, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION:

APPLICANT: La Rosa Thomas J

APPLICANT: Kovalic David K

APPLICANT: Chou Yihua

APPLICANT: Cap Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21 (5323)B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEC TYPES COLORS
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PRIOR FILING DATE: 1998-10-09
PRIOR APPLICATION NUMBER: US 09/615,192
PRIOR FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 407
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 167
LENGTH: 501
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Best Local Similarity
Matches 19; Conserv
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Best Local Similarity
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APPLICANT:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121-1512 CURRENT APPLICATION NUMBER: US/09/833,790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lodes, Michael J.
APPLICANT: Wang, Tongtong
APPLICANT: Secrist, Heather
NUMBER OF SEQ ID NOS: 285684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 495
                                                                                                                                                                                                                                                                                                                                                             1802 TTGATCTGGAGAAAGAATT 1820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            484 TGGTTCAAGGTTTGGCAGG 466
                                                                                                                                                                                                                                                                                                                            10 TTGATCTGGAGAAAGAATT 28
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Mohamath, Raodoh
Indirias, Carol Y.
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100.0%; Fi
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; Pred. No.
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_116754C.1
US-10-424-599-18549
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-23555
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LENGTH: 681
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US-10-027-632-23556/c
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Best Local Similarity
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Publication No. US20030204075A9
Publication No. US20030204075A9
Publication No. US20030204075A9
Publication No. US20030204075A9
PERMERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE FILE 108827.129
FURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FASTSEQ
SEQ ID NO 23555
LENGTH: 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 23555, Application US/10027632 Publication No. US20030204075A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
PILE REFERENCE: 108827.129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
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les 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1745 ТАЛАЛБАТСЛАБАБАБАЛ 1763
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                                                                                                                                                                                                                                                                                                                                                                                                                       82
                                                                                                                                                                                                                                                                                                                                                                                                                    GGAGTTAGCTGAGATGGGG 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.0%; Score 19; DB 15; 00.0%; Pred. No. 48;
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US-10-027-632-23556
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US-10-027-632-11811
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PRIOR PELLING DATE: 2000-07-12
PRIOR PELLING DATE: 2000-04-20
PRIOR PELLING DATE: 2000-04-20
PRIOR PELLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PELLING DATE: 2000-03-29
PRIOR PELLING DATE: 2000-03-29
PRIOR PELLING DATE: 2000-02-24
PRIOR PELLING DATE: 1000-02-24
PRIOR PELLING DATE: 1999-11-23
PRIOR PELLING DATE: 1999-11-3
                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-11811
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LENGTH: 696
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 10887.129
FILE REFERENCE: 10887.129
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PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
                                                                                                                                                                                                                                               SEQ ID NO 11811
LENGTH: 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1999-08-09
                                                                                                          Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
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                            1491 CAGGGAAGAGATGGATGCA 1509
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  579 CAGGGAAGAGATGGATGCA
                                                                                          al Similarity
19; Conserva
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                                                                                               Conservative
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                                                                                                                  1.0%; Score 19;
100.0%; Pred. No.
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Pred. No.
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                                                                                                 Mismatches
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                                                                                                                                              DB 15; Length 824;
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                                                                                                      Indels
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RESULT 14 US-10-027-632-11812 Commence 11812, Ap

Application US/10027632

Publication No. US20030204075A9

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US-10-369-493-24736

Sequence 24736, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Blater, Steven C.

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Xianfeng
                                                                                                                                                                                                           TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 24736
LENGTH: 1137
TYPE: DNA
ORGANISM: Methanococcus jannaschii
US-10-369-493-24736
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SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 11812
LENGTH: 824
TYPE: DNA
GRGANISM: Human
US-10-027-632-11812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILLING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1909-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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SUMMARIES

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ALIGNMENTS

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New SGS3 gene from Arabidopsis thaliana, useful for increasing virus resistance in plants and, when inhibited, for increasing transgene expression.

(AVET)

AVENTIS CROPSCIENCE SA.
INST NAT RECH AGRONOMIC

AGRONOMIQUE. Vaucheret H;

Beclin C,

Elmayan T,

WPI; 2001-159529/16. N-PSDB; AAF25374.

Claim 8; Fig 1; 36pp; French.

The present sequence represents an Arabidopsis thaliana SGS3 polypeptide. The SGS3 gene is essential for post-transcriptional inactivation (degradation of RNA) and for resistance to viruses. Overexpression of SGS3 results in plants with increased resistance to viruses, while inactivation of SGS3 in transgenic plants (e.g. by expressing antisense RNA, by mutation or by homologous recombination) increases the level of the transgene product. This product may e.g. impart resistance (to herbicide, insects or pathogens), alter contents of essential fatty acids or proteins, or is pharmaceutically active, e.g. an immunoglobulin or interferon

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                                                                                                                                                                                 orm bacterium; a acid synthesis.
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milarity 100.0%;
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Pred. No. 0;
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ARESULT 3
AAB7917 ID AAB79
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Best Local S
Matches 9
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, pattericularly L-lysine. The present sequence is a protein described in the particularly L-lysine. The present sequence is a protein described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakagawa
Tateishi
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                                                                                                                                                                                                                                                                                                                                                                          Corynebacterium glutamicum; homeostasis; adaptation; HA protein; fine chemical production; organic acid; proteinogenic amino acid; nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside; nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol; carbohydrate; aromatic compound; vitamin; cofactor; polyketide; enzyme; diagnosis; Corynebacterium diphtheriae; genetic engineering;
25-JUN-1999;
08-JUL-1999;
09-JUL-1999;
09-JUL-1999;
09-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corynebacterium
                                                                                                                                                                                                        04-JAN-2001.
                                                                                                                                                                                                                                                                                                         Corynebacterium
                                                                                                                                                                                                                                                                                                                                                               Brevibacterium;
                                                                                                                                                       23-JUN-2000;
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DB; AAH66753.
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9; Conserva
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; 2000JP-00159162.
; 2000JP-00280988.
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Senoh A,
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ilarity 100.0%;
Conservative
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     99US-0141031P.
99DE-01031636.
99DE-01032125.
99DE-01032126.
99DE-01032127.
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Ikeda M,
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%; Pred. No. 2.6
0; Mismatches
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Ozaki A;
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RESULT 4
AAB18189
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                                                                                                                                                                                                                                                                           CC AAF71138 to AAF71357 encode the Corynebacterium glutamicum homeostasis CC and adaptation (HA) proteins given in AAB79023 to AAB79242. The C. CC glutamicum HA genes (I) can be used in vectors for expression in host CC cells and production of fine chemicals, such as, an organic acid, CC proteinogenic or nonproteinogenic amino acid (preferred), purine or CC pyrimidine base, nucleoside, nucleotide, lipid, saturated or unsaturated CC fatty acid, diol, carbohydrate, aromatic compound, vitamin, cofactor, CC polyketide or enzyme. The amino acids produced can be lysine, glutamine, CC glutamate, alanine, aspartate, glycine, serine, threonine, methionine, CC cysteine, valine, leucine, isoleucine, arginine, proline, histidine, CC tyrosine, phenylalanine, or tryptophan. The fine chemical production can be modulated. The presence of (I) or HA proteins encoded by then are used for diagnosing the presence or activity of Corynabacterium diphtheriae. CC (I) can be used to map the C. glutamicum genome or can be used as markers CC for genetically engineered Corynabacterium or Brevibacterium. The HA CC glutamicum or help the microorganism to adapt to different environmental CC conditions
                                                                                                                                                                                        Matches
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Best Local
               07-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated Corynebacterium glutamicum nucleic acid for production or modulation of production of fine chemicals such as amino acids, nucleosides, nucleotides, lipids, fatty acids, carbohydrates, vitamins or
                                        AAB18189;
                                                                  AAB18189 standard;
                                                                                                                                                                                                                                            Sequence 237
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9; Conserv
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                                                                                                                                    DSDALDDSD
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                                                                                                                                                                                         Conservative
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              (first entry)
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99DE-01033002.
99DE-01033003.
99DE-01033006.
99DE-01033006.
99DE-01041378.
99DE-01041379.
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100.0%; Pr
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                                                                                                                                                                                       Score 9; DB 4; Pred. No. 2.7 0; Mismatches
                                                                  483
                                                                                                                                                                                                     DB 4;
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                                                                                                                                                                                         Indels
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RESULT 5
ABU23489
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AC ABU2
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DT 19-J
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DE Prot
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                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                   Query Match
Best Local
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(CARU/) CARUCCI D.
(GARD/) GARDNER M.
(VENT/) VENTER J C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteins encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum, useful as antimalarial vaccines and in the diagnosis of P.falciparum infection.
                 Protein encoded by Prokaryotic essential gene #9016.
                                                  19-JUN-2003
                                                                                   ABU23489
                                                                                                                   ABU23489 standard; protein; 916
                                                                                                                                                                                                                                                                                                                                      Sequence 483 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 112-113; 577pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-365347/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum; antimalaria; malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum chromosome 2 related protein SEQ ID NO:46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hoffman S, Carucci
                                                                                                                                                                                                     33
                                                                                                                                                                                                                        47 ISKKNKNK 54
                                                                                                                                                                                                                                                                  8; Conserve
                                                                                                                                                                                                     ISKKNKNK 40
                                                                                                                                                                                                                                                                     Conservative
                                                  (first entry)
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                                                                                                                                                                                                                                                                  1.3%; Score 8;
100.0%; Pred. No.
rative 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome 2;
protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gardner M,
                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter JC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human malaria parasite; vaccine; infection; insecticide.
                                                                                                                                                                                                                                                                            DB 55;
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                                                                                                                                                                                                                                                                                                     Length 483
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The invention relates to an isolated nucleate action where expression countries in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are: of the mucleic acid inhibits proliferation of a cell. Also included are: consider a vector comprising a promoter operably linked to the mucleic acid (1) a vector comprising a promoter operably linked to the mucleic acid (2) a host cell containing the vector; (3) an isolated mucleic acid; (4) an antibody capable of specifically binding contingent whose expression is inhibited by the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular contingents and provide acid; (4) an antibody capable of specifically binding the polypeptide; (6) producing the polypeptide; (6) inhibiting cellular contingents and provide a compound that influences the activity of proliferation; (7) identifying a compound that influences the activity of required for proliferation, or that inhibits cellular proliferation; (8) required for proliferation, or that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound that inhibits proliferation of an organism. The antibiotic; (10) profiling a compound that inhibits proliferation of the strains; or (13) identifying the target of a compound that inhibits the contingents acts of the strains is present in a culture or collection of contingents and contingents and contingents are useful for cellular proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation to isolate candidate molecules for rational contingents of a cardiate molecules for rational contingents of the princed specification, but was obtained contingents of the princed specification, but was obtained contingents of the princed specification, but was obtained contingents of the princed specification, but was obtained contingents of the princed specification, but was obtained contingents and contingents and contingents and contingents and contingents and c
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Best Local S
Matches 8
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06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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Wall
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antisense nucleic acids, useful for identifying proteins or screening homologous nucleic acids required for cellular proliferation to late candidate molecules for rational drug discovery programs.
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DB; ACA27359.
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654
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Trawick
                                                                         8
                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prokaryotic essential gene; cell proliferation; drug design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 51413; 1766pp; English
                                                                                                                                                                                       int/pub/published_pct_sequences
FDEALEQL
                                   FDEALEQL 614
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Carr (
                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an isolated nucleic acid comprising any
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                                                                             score 8; DB 6; Pred. No. 96; 0; Mismatches
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                                                                                                 DB 6;
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Forsyth RA,
                                                                                                                   Length 916;
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Xu HH;
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Sequence 1553 AA;

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RESULT 6
ADC9906X
XX ADC990X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADC99064 standard; protein; 1553 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's; diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan; helminthic infection; transgenic; gene therapy; human; enzyme.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ramkumar J,
Thornton MB,
Zebarjadian '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-OCT-2001; 2001US-0345474P.
02-NOV-2001; 2001US-034391DF.
13-NOV-2001; 2001US-033939BP.
16-NOV-2001; 2001US-0334248P.
30-NOV-2001; 2001US-0334288P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-OCT-2002; 2002WO-US033723.
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                                                                                     The invention relates to a novel isolated polypeptide which is a hums kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides, agonists and antagonists are useful for diagnosing, treating or preventing cell proliferative disorders such as atherosclerosis, hepatitis and cancer, developmental disorders e.g. mental cirrhosis, hepatitis and cancer, developmental disorders such as a parkinson's disease, autoimmune and inflammatory disorders such as parkinson's disease, autoimmune and inflammatory disorders such as parkinson's disease, autoimmune and inflammatory disorders such as parkinson's disease, autoimmune and inflammatory disorders such as parkinson's disease, autoimmune and inflammatory disorders such as parkinson's disease and diabetes mellitus and finally, viral, bacterial, fungal, parasitic, protozoan or helminthic infections. Furthermore, to polynucleotides encoding KPP may be useful for creating transgenic animals to model human disease, as wall as during gene therapy procedures. The current sequence is that of the human KPP protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human kinases and phosphatases and polynucleotides, useful for diagnosing, treating or preventing autoimmune or inflammatory disorders (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis, cancer or hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADC99116
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Lindquist EA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID
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Recipon SA, Richardso
, Tran UK, Chawla NK,
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Hafalia AJA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO 17; 424pp; English
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he IJ, Gandhi AR, Gorvad AB, Griir
a AJA, Khan FA, Lal PG, Lee BA, I
M, Lu Y, Marquis JP, Nguyen DB,
M Richardson TW, Swarnakar A,
n SA, Richardson TW, Swarnakar A,
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E, Griffin
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Yao MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arvizu CS;
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                                                                                                                      protein of the
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Best Local Similarity
Thes 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; kinase polypeptide; PKIN-20; gene therapy; Addison's disease; leukaemia; immune disorder; lymphoma; melanoma; developmental disorder; acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension; asthma; Crohn's disease; rheumatoid arthritis; bursitis; atherosclerosis; cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer; cholestasis; anti-HIV; cardiovascular disorder; Niemann-Pick's disease; lipid disorder; fatty liver; Gaucher's disease; myocardial infarction; drug screening; transgenic animal; antiinflammatory; hepatotropic;
New human kinase polypeptide, useful in diagnosis, prevention and treatment of cancer, immune disorder, growth and developmental dicardiovascular disorder and lipid disorder.
                                                                                                                                                                              Tribouley CM, Ba
Yao MG, Elliott
Tang YT, Xu Y,
                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-2000; 2000US-0220038P.
28-JUL-2000; 2000US-0222112P.
04-AUG-2000; 2000US-0222831P.
11-AUG-2000; 2000US-0224729P.
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                                                                                                     WPI; 2002-206083/26.
N-PSDB; AAD30567.
                                                                                                                                                                                                                                                                                 Thornton M,
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                                                                                                                                                                                                                                                                                                                                    THORNTON M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide
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                                                                                                                                                                        Yue H, Khan FA, Gururajan R, Hafalia AJA, Walia N
Ramkumar J, Gandhi AR, Policky JL, Baughn MR;
Bandman O, Nguyen DB, Lu Y, Burford N, Lal P,
ott VS, Recipon SA, Kearney L, Lu DAM, Greenwald
Y, Walsh RT, Gietzen KJ, Yang J, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "CNH domain"
1100. .1380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for diagnosing, treating and preventing cancer (e.g., leukaemia, lymphoma, melanoma), an immune discrete (e.g., acquired immunodeficiency syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's disease, rheumatoid arthritis), a growth and developmental disorder (e.g. bursitis, cirrhosis, hepatitis, psoriasis, Cushing's syndrome), a cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial infarction), and a lipid disorder (e.g., fatty liver, cholestasis, Gaucher's disease, Niemann-Pick's disease). PKIN is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. PKIN is useful for creating knockin humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in the Chromosomal location due to translocation, inversion, etc., among normal, carrier or affected individuals, and as hybridisation
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Best Local
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                                                  New human prostatic specific membrane antibody protein 11.88 polypeptide for treating e.g. prostatic cancer, folic acid metabolic fault, human
                                                                   New human
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                                                                                                                                                                                                               06-NOV-2000; 2000CN-00127237.
                                                                                                                                                                                                                                                  06-NOV-2000; 2000CN-00127237.
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                                                                                                                                                                                                                                                                                                                         CN1352107-A
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                              haemopathy; human immunodeficiency virus; HIV; immunological disease; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                Human; prostatic specific membrane antibody protein 11.88; antibody; prostatic cancer; prostatic benign tumour; folic acid; metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prostatic specific membrane antibody protein 11.88 N-terminal peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 170-174; 196pp; English
                                                                                                                                                                               (BODE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G protein-coupled receptor; GPCR; antigenic peptide; gene therapy; g protein-coupled receptor modulator; antibody; immune-related disease; growth-related disease; cell regeneration-related disease; AIDS; cancer; immunological-related cell proliferative disease, autoimmune disease; Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy; osteoporrosis; cardiomyopathy; inflammation; Crohn's disease; diabetes; graft versus host disease; Parkinson's disease; multiple solerosis; pain; psoriasis; anxiety; depression; schizophrenia; dementia; memory loss; mental retardation, epilepsy; asthma; tuberculosis; obesity; nausea; mental retardation, epilepsy; asthma; tuberculosis; obesity; nausea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP82841 standard; peptide; 18
The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity c
                                                                                                                                                                                     Claim 1; Fig
                                                                                                                                                                                                                                                     autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burmer GC,
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                                                                                                                                                                                                                                                                     w isolated antigenic peptides e.g., for G protein-coupled receptors PCR), useful for diagnosing and designing drugs for treating conditions which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
                                                                                                                                                                                                                                                                                                                                                                                                 2003-046718/04.
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                                                                                                                                                                                     2; 523pp;
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100.0%; Pr
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Example 1;

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95pp; English transcription

patent

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RESULT 10
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Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                        New transcription transactivator protein of CITED family, termed HCITEDX, useful for controlling hypoxia signaling, inflammation, activating cholesterol uptake genes and identifying compounds interfering with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 angiogenesis; atopic disease; cytostatic;
p35srj/CITED2 p300-CH1 interacting domain.
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                                                                                                                                                                                                                                                                                      N-PSDB; AAI84398
                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT,
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18-MAY-2000; 2000US-00577409
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                                                                                                                                                     Isolated nucleic acids and polypeptides, and treating e.g. leukemia, inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth factor; immunomodulatory; cancer; le system disorders; arthritis; inflammation.
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                                                                                                                                                          useful for preventing diagnosing and immune disorders.
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The invention relates to human polynucleotides (AAI79941-AAI93841) and

Claim 20; SEQ ID NO 18359; 1399pp + Sequence Listing; English

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RESULT 1:
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Matches 7; Conser
The present sequence is conserved protein region of a Caenorhabditis elegans homologue of a key metabolic enzyme. A number of C. elegans genes have been identified as homologues of genes in the mammalian insulin signalling pathway. The C. elegans age-1 gene encodes a homologue of the mammalian PI 3-kinase whilst daf-2 encodes a homologue of the mammalian risulin receptor. The C. elegans AKT kinase and PKB kinase act downstream of daf-2 and age-1, just as their mammalian homologues act downstream of insulin signalling. The C. elegans PTEN lipid phosphatase homologue, DAF-18, has been found to act upstream of AKT in the pathway. This discovery has enabled mammalian PTEN action to be mapped to the insulin signalling pathway. Conserved DAF motifs can be used to design probes to identify mammalian DAF homologues and thus to identify individuals with a predisposition toward the development of glucose intolerance conditions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activiny, interest growth factor activity, immunomodulatory activity and activiny inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 167; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diagnosing and treating obesity and impaired glucose tolerance using modulators of daf-18 expression and/or activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans; metabolic enzyme; AKT kinase; daf-18; insulin signalling pathway; daf-2; age-1; insulin receptor; PI 3-kinase; PKB kinase; PTEN lipid phosphatase; antidiabetic; anorectic; obesity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rotavirus; non-structural protein 4; NSP4; protein coordinate data; crystal structure; antiviral; vaccine; diarrhoea; gastroenteritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine rotavirus non-structural protein 4 NSP4 fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the crystal structure of the oligomerisation domain of the rotavirus non-structural protein 4 (NSP4). Rotavirus is a major cause of gastroenteritis, and the structure can be used to construct peptides useful in vaccines to protect against infection. The present sequence is a fragment of a rotavirus NSP4 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel crystal of oligomerization domain of rotavirus nonstructural protein 4, useful for determining 3 dimensional crystal structure of the domain that is used for identifying agents which interact with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 1B; 81pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the crystal structure of the oligomerisation domain of the rotavirus non-structural protein 4 Rotavirus is a major cause of gastroenteritis, and the structure used to construct paptides useful in vaccines to protect against infection. The present sequence is a fragment of a rotavirus NSP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-NOV-2001;
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                        21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                  SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
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Search completed: April 6, 2004, 19:42:00 Job time : 62 secs
                                                                                                                                                                                                                                                                                                                                                Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic CC polypeptides. The proteins and their associated DNA sequences are used in CC the treatment, prevention and diagnosis of medical conditions caused by CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. CC P. acnes is also involved in infections of bone, joints and the central CC nervous system, however it is particularly involved in the inflammatory CC lesions associated with acne vulgaris. A method for detecting the CC presence or absence of P. acnes in a patient comprises contacting a CC sample with a binding agent that binds to the proteins of the invention CC and determining the amount of bound protein in the sample. The CC polypeptides may be used as antigens in the proteins of the invention CC polypeptides may be used as antigens in the production of antibodies Gerific for P. acnes proteins. These antibodies can be used to CC downregulate expression and activity of P. acnes polypeptides and CC diagnostic agents for determining P. acnes proteins may also be used as CC diagnostic agents for determining P. acnes presence, for example, by CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for this patent did not form part of the printed specification, but was CC obtained in electronic format directly from WIPO at
                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                     Sequence 51 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
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N-PSDB; AAS59521.
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L'maisonneuve J, Zhang Y,
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GenCore version 5.1.6 (c) 1993 - 2004 Compus

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ALIGNMENTS

R;Maggi, L.; Scheet, P.; Dubbelde, C. submitted to the EMBL Data Library, October 1998 A;Description: The sequence of C. elegans cosmid C39F7. A;Reference number: Z21407 A;Accession: T33782 hypothetical protein ZK546.13 - Caenorhabditis elegans (;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T27901 R;Hallsworth, K. submitted to the EMBL Data Library, June 1995 A;Description: The sequence of C. elegans cosmid ZK546. A;Reference number: Z20437 Query Match Best Local Similarity Whiches 9; Conserva A; Molecule type: DNA A; Residues: 1-603 <HAL A; Cross-references: EMBL: UZ9380; PIDN: AAA68747.1; CESP: ZK546.13 A; Experimental source: strain Bristol N2 C; Genetics: RESULT 1 T27901 A; Map position: 5 A; Introns: 14/2; 45/3; 224/1 C; Superfamily: Caenorhabditi A;Cross-references: EMBL:AF101310; PIDN:AAC69214.1; GSPDB:GN00023; CESP:C39F7.5 A;Experimental source: strain Bristol N2; clone C39F7 C;Genetics: A;Gene: CESP:C39F7.5 A; Molecule type: DNA A; Residues: 1-353 < MAG> hypothetical protein C39F7.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
C;Accession: T33782 A;Accession: T27901 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A; Gene: CESP: ZK546.13 A; Introns: 26/3; 111/: Query Match 469 LEIMSEKLR 477 433 LEIMSEKLR 441 26/3; 111/3; 196/3; 275/3; 331/1; 362/3; 438/3; 500/3 Caenorhabditis elegans hypothetical protein C39F7.5 Conservative 100.0%; +1 1.4%; Score 9; DB 1 100.0%; Pred. No. 1.5 ive 0; Mismatches 1.3%; Score 8; DB 2; DB 2; lo. 1.5; Length 353; Length 603; <u>.</u> Indels 0 Gaps 0

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein PFB0235w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Pate: 13-NOV-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
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A;Experimental source: clone 3D7
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
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A;Introns: 158/3; 269/3; 354/3; 493/2; 538/2
A;Introns: Caenorhabditis elegans hypothetical protein C18E9
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: T19406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, March 1996 A; Reference number: {\tt Z19120}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T19406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
snRNP homolog (imported) - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001
C;Accession: G84303
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                                                                                                                                                                                                                                                                                                                                                                A, Experimental source: clone C18E9
                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:Z70034; PIDN:CAA93857.1; GSPDB:GN00020;
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                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
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Matches
                                                                     G84303
                                                                                       RESULT 5
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Best Local S
Matches 8
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Best Local
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8; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                      1-586 <WIL>
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8; Conserv
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                                                                                                                                          RELAEVLE
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ilarity 100.0%;
Conservative 0
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100.0%; Pred. No. 16;
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Pred. No.
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                       02-Feb-2001 #text_change 02-Feb-2001
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                                                                                                               A;Title: The complete genome of the hyperthermophilic bacterium A;Reference number: A70300; MUID:98196666; PMID:9537320 A;Accession: B70456
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                                               A;Molecule type: DNA
A;Residues: 1-135 <AQF>
A;Cross-references: GB:AE000757; NID:g2984092; PIDN:AAC07635.1;
                A;Experimental source: strain VF5 C;Genetics:
                                                                                              A;Status: preliminary; nucleic acid sequence not shown; translation not
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G.; Warren, P.V.; Gaasterland,

T.; Young,

₩.G.;

Lenox,

A.L.; Graham,

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Aquifex aeolicus

PID:g2984097; GB:AE00065

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Jung, K.H.; Alam, M.; Freitas, T.
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: G84303
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A;Gene:
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
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A;Residues: 1-69 <STO>
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C; Superfamily: Ha
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C;Genetics:
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A; Residues: 1-101 <STO>
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Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor
thioredoxin - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: B70456
C;Accession: B70456
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7; Conserve
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                                                                 Aquifex aeolicus
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100.0%; Pred. No.
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).G.; Jablor
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ster, B.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AI2869
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J. Bacteriol. 183, 4823-4838, 2001.
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: C97338
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A;Residues: 1-145 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL43375.1; PID:g17740871; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                        erage, G.; Gliter, T., Carally, S.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
Science 294, 2317-2323, 2001
Stanthors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
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A;Molecule type: DNA
A;Residues: 1-141 <KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TP pyrophosphohydrolase, MutT family [imported] - Agrobacterium tumefaciens;Species: Agrobacterium tumefaciens;Date: 11.Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002;Date: 11.Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Cross-references: GB:AE001437; PIDN:AAK81494.1; PID:g15026667; GSPDB:GN00168;Experimental source: Clostridium acetobutylicum ATCC824
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les 7; Conserv
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                                                               LHRELAE 266
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                       LHRELAE 57
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100.0%; Pred. No. 50;
Live 0; Mismatches
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                                                                                                                        DB 2;
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o. 47;
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A;Cross-references: EMBL:M10138; NID:g171294; PIDN:AAA66900.1; PID:g171295
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C;Species: Saccharomyces cerevisiae
C;Date: 13-Jun-1983 #sequence revision 31-Dec-1992 #text_change
C;Accession: A22853; S46730; A00494; S48874
R;Wright, R.M.; Ko, C.; Cunsky, M.G.; Poyton, R.O.
J. Biol. Chem. 259, 15401-15407, 1984
A;Title: Isolation and sequence of the structural gene for cytoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X64765; NID:g40798; PIDN:CAA46012.1; A;Experimental source: strain AFCC 29494 C;Superfamily: flavodoxin; flavodoxin homology C;Keywords: electron transfer; flavoprotein; FMN F;6-143/Domain: flavodoxin homology <FLX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE007869; PIDN:AAK88124.1; PID:g15157558; GSPDB:GN00169 C;Genetics: C.;Genetics: A;Gene: AGR C 4330 A;Map positTon: circular chromosome
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Biochim. Biophys. Acta 1131, 325-328, 1992
A;Title: The primary structures of the flavodoxins from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      flavodoxin - Desulfovibrio gigas (ATCC 29494)
C;Species: Desulfovibrio gigas
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 05-May-2000
C;Accession: S24310
A; Molecule type: DNA
A; Residues: 1-148 < WRI>
                                                                                                                                                                                                                                       cytochrome-c oxidase (EC 1.9.3.1) chain VI precursor - N.Alternate names: protein H8179.2; protein YHR051w
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A; Residues: 1-147 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-147 <HEL>
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                                                A;Accession: A22853
                                                                  A; Reference number: A92466; MUID: 85080033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 294, 2323-2328, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, N.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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Best Local
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7; Conserva
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Conservative
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100.0%; Pred. No.
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; Lappas, C.; Markelz,
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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C;Accession: D6983
C;Accession: D6983
C;Accession: D6983
C;Accession: D6983
C;Browlst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V; Berter R;Kunst, F; Ogasawara, N; Moszer, I; Albertini, A.M.; Alloni, G; Azevedo, V; Catter, N.M.; Chc C; Bron, S; Broullet, S; Bruschi, C.V.; Caldwell, B; Capuano, V; Catter, N.M.; Chc C; Ebraic, A.; Ebrich, S; Bruschi, C.Y.; Entian, K.D.; Errington, J; Fabret, C.; Ferrari, E. A.; Ebrich, S; D; Emmerson, P.T.; Entian, K.D.; Errington, J; Fabret, C.; Ferrari, E. A.; Althors: Soulger, D; Fritz, C.; Fujita, M.; Fujita, Y; Fuma, S; Galizzi, A.; Galler A; A; Hibert, H.; Holsappel, S; Hosono, S.; Hullo, M.F.; iech, J.; Karnita, K.; Lapidus, A.; Lardinois, Koetter, P.; Koningstein, G; Kroph, S; Kumano, M; Kurita, K.; Lapidus, A.; Lardinois, Koetter, P.; Koningstein, G; Kroph, S; Kumano, M; Kurita, K.; Lapidus, A.; Lardinois, Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Y, M.; Schleich, S.; Schroeter, R.; Scoffene, F; Sekiguchi, J.; Sekowska, A.; Serot, A; Winters, P.; Winters, P.; Winters, P.; Winters, P.; Yanamoto, H.; Yanamoto, H.; Yasumoto, K.; Yasumoto, K.; Yasumoto, V.; Uchiyama, A; Minters, P.; Winters, P
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J. Biol. Chem. 257, 13081-13087, 1982
A;Title: The amino acid sequence of cytochrome c oxidase
A;Reference number: A00494; MUID:83030850; PMID:6290493
A;Accession: A00494
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A; Reference number: S46732
A; Accession: S46730
A; Molecule type: DNA
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Nucleic Programmer of the COX6 genetic locus A;Title: Organization and expression of the COX6 genetic locus A;Reference number: S48872; MUID:89160242; PMID:2537949
A;Accession: S48874
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A; Residues: 1-148 < DUZ>
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A; Residues: 41-148 < GRE>
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A;Map position: 8R
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A;Residues: 1-23 <WRW>
A;Cross-references: EMBL:X14452; NID:g3573; PIDN:CAA32622.1;
C;Comment: Cytochrome-c oxidase is the terminal component of
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7; Conserve
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he sequence of S. cerevisiae
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0; Mismatches
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A;Gene: yhfO
C;Superfamily: Methanococcus jannaschii
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Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C. A;Authors: Kahn, D.; Kahn, M. Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, C. A;Authors: Kahn, D.; Kahn, M.; Vorholter, F.J.; Weidner, S.; Weils, D.H.; Wong, C. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A;Reference number: A96039; MUID:21368234; PMID:11474104
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A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endomore in the complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-fixing endomore in the N2-
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C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
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A;Molecule type: DNA
A;Residues: 1-152 <KUR>
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A;Genome: plasmi
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A;Gene: CESP:T23C6.4
A;Map position: X
A;Introns: 37/1; 90/1; 142/2
C;Superfamily: Caenorhabditis
                                                                                                                                                                    A;Cross-references: EMBL;AF000191; NID:g1946976; PID:g1946981; A;Experimental source: strain Bristol N2; clone T23C6
                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-182 < DUZ >
                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, April 1997
A,Description: The sequence of C. elegans cosmid T23C6
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; Fisher, R.F.,
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Search completed: April 6, 2004, 19:44:01 Job time : 22 secs	Db 173 GRGNGNG 179	Qy 94 GRGNGNG 100	Matches 7; Conservative 0; Mismatches	Query Match 1.1%; Score 7; DB 2; Length 182;
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CCX6_YEASTI
G6PD_SARBU
NT3_CTREL
X370_THEMAN
NT3_FELCA
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NT3_HOUSE
CTI72_HUMAN
YNR3_AZORR
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Optst2 felis silve
P20783 homo sapien
P20181 mus musculu
P18280 rattus norv
O35740 mus musculu
O9967 homo sapien
P45674 azospirillu
O8fi04 escherichia
P24209 escherichia
                                                                   O9zjj7 helicobacte
Q9ukp3 homo sapien
Q8uin5 agrobacteri
O92st0 rhizobium m
P54918 synechocyst
Q87s16 vibrio para
Q8dez8 vibrio vuln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q97da9 clostridium
Q01096 desulfovibr
P00427 saccharomyc
Q25537 sarcophaga
Q95150 cervus elap
Q9wyk4 thermotoga
P25433 gallus gall
Q7v6b8
060478
Q7vga7
                                                                                                                                                                                                                                  059823
P32773
P32814
P35693
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Q8eqt9 oceanobacil
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99 escherichia
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TABPA_OCEIH STANDARD; PRT; 113 AA.

GBEQT9;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ribosome-binding factor A.

RBFA OR OB1600.

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SULT 2	1 1	Query Match Best Local Matches	EMBL; HAMAP; InterP Pfam; Transc SEQUEN	r node herv	Nakagawa S "Complete Submitted -!- FUNCTI simila -!- SIMILA	Bacteria; Actin Corynebacterine NCBI_TaxID=1718 [1] SEQUENCE FROM N	28-FEB-2003 (Rel. 41, Cre 28-FEB-2003 (Rel. 41, Las 28-FEB-2003 (Rel. 41, Las 28-FEB-2003 (Rel. 41, Las Nutilization substance I NUSB OR CGL1618.			8 8 8 8 8 8 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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SEQUENCE FROM N.A.

STRAIN-HTE831 / DSM 14371 / JCM 11309;

STRAIN-HTE831 / DSM 14371 / JCM 11309;

MEDLINE=22220767; PubMed=12235376;

MEDLINE=22220767; PubMed=12235376;

MEDLINE=22220767; PubMed=12235376;

MEDLINE=22220767;

MEDLINE=22220
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-!- FUNCTION: Associates with free 30S ribosomal subunits (but not with 30S subunits that are part of 70S ribosomes or polysomes).

Essential for efficient processing of 16S rRNA. May interact with the 5'-terminal helix region of 16S rRNA (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AP004598; BAC13556.1; -.

HAMAP; MF 00003; -; 1.

InterPro; IPR000238; Rib_bind_factA.

Pfam; PP02033; RBBA; 1.

ProDom; PD007327; Rib_bind_factA; 1.

TIGRPANG; TIGR00082; rbfA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=182710
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PROSITE; PS01319; Complete proteome.

PRNA processing; Complete proteome.

113 AA; 12924 MW; DACC
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
(3R)-hydroxymyristoyl-(acyl carrier protein)
((3R)-hydroxymyristoyl ACP dehydrase).

FABZ OR CAC3571.
                                                                                                          SEQUENCE FROM N.A.

STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE-21359325, PubMed=11466286;

MODELINE-21359325, PubMed=11466286;

Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeno Noelling J., Wolf Y.I.

Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., I.

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solvent-property of the solven
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                                         J. Bacteriol. 183:4823-4838(2001)
-!- FUNCTION: Involved in saturat
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           nvolved in saturated fatty LOCATION: Cytoplasmic (By
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PROSITE;

PS00201; PS50902;

FLAVODOXIN; 1.
FLAVODOXIN_LIKE; 1.

PRINTS; PR00369; FLAVODOXIN

InterPro; IPR008254; Flav nitox InterPro; IPR001094; Flavdoxin I InterPro; IPR001126; Flavodoxin. InterPro; IPR001256; Flavodoxin. Pfam; PF00258; flavodoxin; 1.

nitox synth. doxin like.

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RESULT 4

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HAMAP; MF 00406; -; 1.
InterPro; IPR006683; Thioestr_supf.
Pfam; PF03061; 4HBT; 1.
Lyase; Lipid synthesis; Lipid A biosynthesis; Complete proteome.
Lyase; Lipid synthesis; Lipid A biosynthesis; Complete proteome.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1993
10-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q01096;
01-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The primary structures of the flavodoxins from two strains besulfovibrio gigas. Cloning and nucleotide sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Desulfovibrio gigas.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochim. Biophys. Acta 1131:325-328(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC 29494 / DSM 496;
MEDLINE=92329549; PubMed=1627649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Deitaprot
Desulfovibrionaceae; Desulfovibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Flavodoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright between the Swiss Institute of Bio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              structural genes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helms L.R., Swenson R.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- COFACTOR: FMN
                                                                                                                                                                                                                                             PIR; S24310; S24310.
HSSP; P00323; 2FX2.
                                                                                                                                                                                                                                                                                                                  EMBL; X64765; CAA46012.1; -.
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sen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the flavodoxin family. SIMILARITY: Contains 1 flavodoxin-like domain.
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MBL outstation -
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                                                                                                  Jaccharomyces cerevisiae.";
J. Biol. Chem. 257:13081-13087(1982).
-!- FUNCTION: This is the heme A-containing chain of cytochrome oxidase, the terminal oxidase in mitochondrial electron tran-
-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricyto
                                                                                                                                                                                                                                                                                                                                                                                                                Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., I Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirste Kucaba T., Hillier L. W., Jer M., Johnston L., Langston Y., Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Ve Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R. Vaudin M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Cytochrome c oxidase polypeptide VI, mitochondrial precursor (EC 19.3.1).
                                                                                                                                                                                                                                                   Wright R.M., Rosenzweig B., Poyton R.O.; "Organization and expression of the COX6 genetic locus in Saccharomyces cerevisiae: multiple mRNAs with different 3 are transcribed from COX6 and regulated differentially."; Nucleic Acids Res. 17:1103-1120(1989).
                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-23 FROM N.A. MEDLINE=89160242; PubMed=2537949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=85080033; PubMed=6210289; Wright R.M., Ko C., Cumsky M.G., Poyton R.O.; Wright R.M., Ko C., Cumsky M.G., Poyton R.O.; "Isolation and sequence of the structural gene for cytochrome oxidase subunit VI from Saccharomyces cerevisiae."; J. Biol. Chem. 259:15401-15407(1984).
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                                                                                                                                                                                                        MEDLINE=83030850; PubMed=6290493;
                                                                                                                                                                                                                         SEQUENCE OF 41-148
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Saccharomycetales; Saccharomycetaceae;
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P00427;
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                                            SUBUNIT: Composed of at least 11 subunits.
SUBCELLULAR LOCATION: Mitochondrial inner of
SIMILARITY: Belongs to the cytochrome c ox
                  SWISS-PROT entry is copyright.
                                                                                                                                                                          or I., Tsugita A.; amino acid sequence of cytochrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23
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    Swiss Institute
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    Bioinformatics
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It is produced through a collaboration informatics and the EMBL outstation
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me c oxidase Va family.
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the

PRINTS; PR00079; G6PDHDRGNASE.
PRODOM; PD001129; G6PD; 1.
PROSITE; PS00069; G6P_DEHYDROGENASE; PARTIAL.
Oxidoreductase; NADP; Glucose metabolism.

InterPro; IPR001282; G6PD

PF00479; G6PD;

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EMBL; U00062; AAB688
EMBL; X14452; CAA326
PIR; A22853; OTBY6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q25537;
15-JUL-1998
15-JUL-1998
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                   Soto-Adames F.N., Robertson H.M., Berlocher S.H.;
"Phylogenetic utility of partial DNA sequences of G6PDH at
taxonomic levels in Hexapoda with emphasis on Diptera.";
Ann. Entomol. Soc. Am. 87:723-736(1994).
-i- CATALYTIC ACTIVITY: D-glucose 6-phosphate + NADP(+) = D
-i- SIMILARITY: Belongs to the glucose-6-phosphate dehydrog
-i- SIMILARITY: Belongs to the glucose-6-phosphate dehydrog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JIL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Glucose-6-phosphate 1-dehydrogenase (F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GermOnline; 139368; -. SGD; S0001093; COX6.
                                                                                                                                       EMBL; U09037;
HSSP; P11411;
                                                                                                                                                                                                                                       entities requires a
                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sarcophagidae; S
NCBI_TaxID=7385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sarcophaga bullata (Grey flesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02284; COX5A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Zwischenferment) (Fragment).
                                                                                                                                                                                                              tities requires a license agreement (S send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO:0005751; C:respiratory chain complex IV (sensu Eukarya); IPI. GO:0004129; F:cytochrome-c oxidase activity; IDA. erPro; IPR003204; Cyt_c_ox5A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                         family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endopterygota; Diptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bullata (Grey flesh fly) (Neobellieria bullata)
Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 AA;
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CYTOCHROME C OXIDAS
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(EC 1.1.1.49)
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Y370 THEMA
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Q95150;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
Cervidae; Cervinae; Cervus.
                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00248; NGF 1; P; PROSITE; PS50270; NGF 2; PA Growth factor; Signal. SIGNAL PROCEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98001474; PubMed-9343309;
Garcia R.L., Sadighi M., Francis S.M., Suttle J.M., Flemi Garcia R.L., Sadighi M., Francis S.M., Suttle J.M., Flemi Garcia R.L., Sadighi M., Francis S.M., Suttle J.M. Sadighi M., Francis S.M., Suttle J.M., Flemi Garcia S.M., Suttle J.M., Suttle J.M., Flemi Garcia S.M., Suttle J.M., Flemi Garcia S.M., Suttle J.M., Suttle 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Neurotrophin-3 precursor (NT-3) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is no removed and for commercial modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/entities requires a license agreement (See http://www.isb-sib.ch/announce/entities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE=Antler;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proprioceptive sensory neurons.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the NGF-beta family.
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002072; NGF.
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153
                               STANDARD;
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BY SIMILARITY.
NEUROTROPHIN-3.
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RESULT 9
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10-OCT-2003 (Rel. 42, I
15-MAR-2004 (Rel. 43, I
Hypothetical UPF0273 Pi
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Jenome sequence of Thermotoga maritima.";

Nature 399:323-329(1999).
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STRAIN=MSB8 / DSM 3109
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P25433;
P25433;
O1-MAY-1992 (Rel. 22, Created)
O1-DEC-1992 (Rel. 24, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Neurotrophin-3 precursor (NT-3) (Neurotrophic Neurotrophic 2) (NGF-2).
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Nelson K.E., Clayton R.A., Gill S.R.,
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PIR; H72384; H72384.
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NP_BIND 30 3
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Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
                                                                                                  MEDLINE=93091238; PubMed=1457809;
Maisonpierre P., Belluscio L., Conover J.C.,
Maisonpierre P., Belluscio BDNF and NT-3.";
"Gene sequences of chicken BDNF and NT-3.";
DNA Seq. 3:49-54(1992).
SEQUENCE OF 194-236 FROM N.A.
MEDLINE-91222573; PubMed-2025430;
Hallboeoek F., Ibanez C.F., Perss
                                                                                                                                                                                                                                                  NCBI_TaxID=9031;
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protein TM0370.
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ATP (POTENTIAL).
26813 MW; 396431D4D5E48837 CRC64;
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                   Persson H.;
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Phasianidae; Phasianinae;
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T 30-MAY-2000 (Rel. 39, Created)

T 30-MAY-2000 (Rel. 39, Last sequence update)

T 16-OCT-2001 (Rel. 40, Last annotation update)

Neurotrophin-3 precursor (NT-3) (Neurotrophic file)

Neurotrophin-3 precursor (NT-3) (Neurotrophic file)
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Felis silvestris catus (Cat).
Tharyota; Metazoa; Chordata; Cra
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FELCA
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SEQUENCE FROM N.A.
MEDLINE=20211727; PubMed=10745216;
Lein E.S., Hohn A., Shatz C.J.;
Lein f.~~mulation of BDNF and NT
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             This
                                 -!- FUNCTION: Seems to promotes the survival of proprioceptive sensory neurons (By similari-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the NGF-beta family.
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PRINTS; PR00268; NGF.
PRODOm; PD002052; NGF; 1.
SMART; SM00140; NGF; 1.
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-I- FUNCTION: Seems to promotes the survival of visceral and
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SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the NGF-beta family.
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                                                         survival of visceral (By similarity).
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01-FEB-1991 (Rel. 17, Created)
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                                                                                                  SEQUENCE FROM N.A.
MEDLINE=90306351; PubMed=2365067;
Kaisho Y., Yoshimura K., Nakaham
                                                                                                                                                                                                                  MEDLINE=91045937; PubMed=2236018; Jones K.R., Reichardt L.F.; "Molecular cloning of a human gen
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=90262727; PubMed=2344409;

ROSENTHAL A., Goeddel D.V., Nguyen T.,

Laramee G.R., Nikolics K., Winslow J.W

"Primary structure and biological acti-
neurotrophic factor.";
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ProDom; PD002052; NGF; 1.
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HSSP; P20783;
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 MEDLINE=91365361; PubMed=1889806;
                 SEQUENCE FROM N.A.
                                                                                       "Cloning
                                                                                                                                                                                                                                                                                                               Neuron
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Natl. Acad. Sci.
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Belluscio L., de la
Yancopoulos G.D.;
PROSITE; PSSO
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MEDLINE=91222573; PubMed=2025430;
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                                                                                                                                                                                           EMBL; X53655; CAA37703.1; -.
EMBL; M37763; AAA59953.1; -.
EMBL; M61180; AAA63231.1; -.
PIR; A36208; C40304.
PDB; LBND; 04-APR-96.
PDB; 1B8K; 09-FEB-99.
PDB; 1B8K; 09-FEB-99.
PDB; 1NT3; 16-JUN-00.
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MEDLINE=95251647;
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Robinson R.C., Radziejewski C., Stuart D.I.,
"Structure of the brain-derived neurotrophic"
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                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         schizophrenia."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res.
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                                                                                GO; GO:0005102; F:receptor binding;
GO; GO:0007267; P:cell-cell signalin
GO; GO:0007267; P:cell-cell signalin
TAS:
GO; GO:0007199; P:neurogenesis; TAS:
GO; GO:0007165; P:signal transductio
Interpro; IPR002072; NGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           proprioceptive sensory neurons.
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Brain and peripheral tissues.
POLYMORPHISM: Variant Glu-76 (frequently reported thought to be associated with severe forms of schi
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Monte S.M., Squinto S., Furth
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                 NGF_1; 1.
NGF_2; 1.
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MEDLINE-90190865; PubMed-2314473;
MEDLINE-90190865; PubMed-2314473;
Mehohn A., Leibrock J., Bailey K., Barde Y.-A.;
"Identification and characterization of a novel growth factor/brain-derived neurotrophic factor Nature 344:339-341(1990).
                                                                                                                                                                                                                                                                      Neurotrophin-3 precursor (NT-3) (Neurotrophic (Nerve growth factor 2) (NGF-2).
                                                                                                                                                                                                                                                                                                 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation updat
                                                                                                                                                                                                                                                                                                                      P20181;
01-FEB-1991
                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                            modified and this statement is not remove the statement is not removed the statement is entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                          -!- TISSUE SPECIFICITY: Brain and peripheral tissues.
-!- SIMILARITY: Belongs to the NGF-beta family.
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5 KNKLSKQ 51
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP;
MGD; QG;
GG; QQ;
GG; QQ;
QG; QQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Nerve
gene structures, distribu
Genomics 10:558-568(1991)
[4]
                                                                                                                                                                                                  MEDLINE=90208301; PubMed=2321006; Maisompierre P.C., Belluscio L., (Lindsay R.M., Yancopoulos G.D.; "Neurotrophin-3: a neurotrophic f. Science 247:1446-1451(1990).
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=90319130; PubMed=2164684;

MEDTIONS P., Ibanez C.F., Ebendal T., Olson L., Persson H.;

"Molecular cloning and neurotrophic activities of a protein with
structural similarities to nerve growth factor: developmental and
topographical expression in the brain.";

Proc. Natl. Acad. Sci. U.S.A. 87:5454-5458(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
30-MAY-2000 (Rel. 39, Last amnotation update)
Neurotrophin-3 precursor (NT-3) (Neurotrophic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00243; NGF; 1.
PRINTS; PR00268; NGF.
ProDom; PD002052; NGF; 1.
SMART; SM00140; NGF; 1.
                                                                              MEDLINE=91365361; PubMed=1889806; Maisompierre P.C., le Beau M.M., J Belluscio L. de la Monte S.M., S Yancopoulos G.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00248; NGF_1; PROSITE; PS50270; NGF_2;
                                                           "Human
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
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GO:0005515; F:protein binding; IPI.
GO:0007420; P:brain development; IMP.
GO:000744; P:epidermal differentiation; IMP.
GO:0007403; P:glial cell fate determination; IMP.
GO:0007422; P:peripheral nervous system development; IMP.
GO:0007422; P:positive regulation of transcription from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ve growth factor OR NTF-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              452 KNKLSKQ 458
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                                        and rat brain-derived neurotrophic factor and neurotrophin-3:
tructures, distributions, and chromosomal localizations.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         norvegicus (Rat).
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                                      distributions, and
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100.0%;
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Rodentia;
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BY SIMILARITY.
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC. ...)
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Pred. No.
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Squinto S.,
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Best Local S
Matches 7
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EMBL; M33968; AAAA1727.1; --
EMBL; M61179; AAA63497.1; --
PIR; A35781; A35781.
HSSP; P20783; 1RRF
                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
DISULFID
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DISULFID
CARBOHYD
                                                                                                                                                                O35740; O35741; O35742; O35743; O55198;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cbp/p300-interacting transactivator 2 (MSG-related
STRAIN=C57BL/6 X DBA;
MEDLINE=98202510; PubMed=9533950;
Dunwoodie S.L., Rodriguez T.A., Beddington R.S.P.;
"Msgl and Mrgl, founding members of a gene family, show
patterns of gene expression during mouse embryogenesis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Evolutionary studies of the nerve growth factor family reveal novel member abundantly expressed in Xenopus ovary."; Neuron 6:484-858 (1991).
-i- FUNCTION: Seems to promotes the survival of visceral and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00268; NGF.
ProDom; PD002052; NGF; 1.
SMART; SM00140; NGF; 1.
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InterPro; IPR002072; NGF.
Pfam; PF00243; NGF; 1.
                                                                                       NCBI_TaxID=10090;
                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00248; NGF_1; PROSITE; PS50270; NGF_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91222573; PubMed=2025430; Hallboeoek F., Ibanez C.F., Perss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 195-237 FROM N.A. STRAIN-Sprague-Dawley; TISSUE
                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Belongs to the NGF-beta family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proprioceptive sensory neurons.
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Brain and p
                                                                                                                                                                                                                                 MOUSE
                                                                                                                                                                                                                                                                                                                  452 KNKLSKQ 458
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                                                                                                                                          OR MRG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC.
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                                                                                                                                                                                                                                                                                                                                                              Score 7;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                    PRT;
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                                                                 AND
                                                                                                                                                                                                                                  269 AA
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5. 37;
  embryogenesis.";
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RESULT 15
CIT2 HUMAN
ID CIT2
AC Q9996
DT 15-DE
DT 28-FE
DT 10-OC
DE COP/J
DE COP/J
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GN CITELE
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[2]
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MEDLINE=98094278; PubMed=9434189;
                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Bioinformatics Institute. There are no restrictions on its the Buropean Bioinformatics Institute. There are no restrictions on its the by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shioda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 204:235-241(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         shioda T., Fenner M.H., Isselbacher K.J.; was a transcription activating _{\rm mMSG1} and its related protein MRG1 share a transcription activating
                                                                                                                                                                                                                                                                                                                                                     EMBL; Y15163; CAA75432.1; --
EMBL; Y15163; CAA75433.1; --
EMBL; Y15163; CAA75434.1; --
EMBL; Y15163; CAA75435.1; --
EMBL; Y15163; CAA75435.1; --
EMBL; U86445; AAC39945.1; --
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                  CIT2 HUMAN

CIT2 HUMAN

CIT2 HUMAN

CIT2 HUMAN

CIT2 HUMAN

STANDAY

O99967; O95426;

O99967; O95426;

15-DEC-1098 (Rel. 37, Created)

16-DEC-1093 (Rel. 41, Last sequence update)

10-CCT-2003 (Rel. 42, Last annotation update)

10-CCT-2003 (Rel. 42, Last annotation update)

10-cct. 10 (MSG-related protein company)
                                                                                                                                                                                                                                                                                                                 Pfam;
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                                                                                        HUMAN
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                                                                                                                                                                                                                                                                   VARSPLIC
              protein) (P358
CITED2 OR MRG1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Interferes with the binding of transcription HIF-la and STAT2 to p300/CBP (By similarity). SUBCULIT: Binds to the p300/CBP CH1 region (By similarit SUBCELLULAR LOCATION: Nuclear ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=035740-4; Sequence=VSP 001092; SIMILARITY: Belongs to the CITED family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                     GO:0007417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dev.
                                                                                                                                                                                                                                                                                                                                     MGI:1306784; Cited2.
GO:0007417; P:central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=035740-2; Sequence=VSP_001090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=035740-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=035740-3;
                                                                                                                                                   378
                                                                                                                               233
   sapiens (Human)
                                                                                                                                                                    Similarity 7; Conserv
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162
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                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                               regulation; Nuclear protein;
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/FTId=VSP 001090.

/FTId=VSP (in isoform 3).
                                                                                                                                                                                 Score 7;
; Pred. No
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                                                                                                                                                                                                                     Missing (in isoform 4).
/FTId=VSP_001092.
                                                                                                                                                                                                                                                                                 ASP/GLU-RICH
                                                                                                                                                                                                             FTId=VSP_001092.
AFACDDD5D7902A48 CRC64;
                                                                                                                                                                        Mismatches
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                                                                                                                                                                                   DB 1;
o. 39;
                                                                                                                                                                                                                                                                                                                                          development; IMP
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                                        (MRG1
                                                                                                                                                                             Gaps
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SEQUENCE FROM N.A. (180FORM 2).

MEDLINE=97057236; PubMed=8901575;

Shioda T., Fenner M.H., Isselbacher K.J.;

Shioda T., Fenner M.H., Isselbacher encodes a "msg1, a novel melanocyte-specific gene, encodes a and is associated with pigmentation.";

proc. Natl. Acad. Sci. U.S.A. 93:12298-12303(1996).
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Mammalia; Eutheria;
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transactivation by HIF-1.";
Genes Dev. 13:64-75(1999).
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MEDLINE=99104162; PubMed=9887100;
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                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way use by non-profit institutions as long as its content is in or way and for commercial modified and this statement is not removed. Usage by and for commercial
EMBL; U65093; AAC51114.1; -.
EMBL; AF129290; AAF01263.1; -.
EMBL; AF129290; AAF01264.1; -.
                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                            or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Binds to the p300/CBP SUBCELLULAR LOCATION: Nuclear ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                         INDUCTION: By hypoxia and deferoxamine. SIMILARITY: Belongs to the CITED family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative
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Primates; Catarrhini; Hominidae; Homo.
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DR EMBL; AP109161; AAD10055.1; -.

DR EMBL; BC004377; AAH04377.1; -.

DR Genew; HGNC:1987; CITED2.

DR MIM; 602937; -.

DR GO; GO:0005634; C:nucleus; NAS.

DR GO; GO:0005515; P:protein binding; NAS.

DR GO; GO:0005515; P:regulation of transcription from Pol II pro. ..; TAS.

DR GO; GO:000570; F:transcription factor activity; TAS.

DR GO; GO:0005357; P:regulation of transcription from Pol II pro. ..; TAS.

DR GO; GO:0005376; CITED.

DR InterPro; IPR007576; CITED.

DR FITHOUGHAIN 162 199 HIS-RICH.

FIT DOMAIN 162 199 GILY-RICH (ACIDIC).

FIT DOMAIN 162 199 ASP/GIU-RICH (ACIDIC).

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FIT DOMAIN 219 258 ASP/GIU-RICH (ACIDIC).

FIT DOMAIN 162 199 611 84 45DDE3A9E2B4C472 CRC64;

Query Match 1.1%; Score 7; DB 1; Length 270;

Best Local Similarity 100.0%; Pred. No. 39;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: April 6, 2004, 19:42:29

Job time: 20 secs
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Q7xye6 triticum ae
Q7xy17 triticum ae
Q7x144 caenorhabdi
Q8fq52 corynebacte
Q98bt9 rhizobium 1
Q8g635 bifidobacte
Q7wep5 bordetella
Q7w3c6 bordetella
Q7w3c6 bordetella
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Q8zzm7 pyrobaculum
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EMBL; AF239719; AAF73960.1; ---
EMBL; BT002944; AA022757.1; ---
EMBL; BT004380; AA042374.1; ---
InterPro; IPR005380; XS.
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i submitted (SEP-2002) to the EMBL/GenBank/DDBJ dat

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
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SIRAINacov. PH 82-2-2;
Li J.R., Wang F., Li Q.Z., Zhang X.S.;
Li J.R., Wang F. Li Q.Z., Zhang X.S.;
"Gene isolation and expression of a new Zn-finger.";
"Gene isolation and expression of a new Zn-finger.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF469493; AAP80610.1; -.
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Q7Z144;
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Triticeae; Triticum.
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Q8FQ52;
01-MAR-2003
                                                                                                                                                                                                 "The entire genomic sequence of Corynebacterium Submitted (MAY-2002) to the EMBL/GenBank/DDBJ da EMBL; AP005218; BAC18092.1; -.
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H.
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi
Usuda Y., Sugimoto S.;
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01-MAR-2003
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Rhabditidae; Peloderinae;
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STRAIN=Bristol N2;
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MEDLINE=99069613; PubMed=9851916;
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01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterineae; Corynebacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CBI_TaxID=152794;
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             Similarity 9; Conserv
                                                                                                                                                                    proteome.
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                                                                                                                                          321 AA;
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(TrEMBLrel. 23, Last sequence up
(TrEMBLrel. 23, Last annotation
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         Score 9; DB 1; Pred. No. 1.9
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elegans Sequencing Consortium.";
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Matches
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Bifidobacteria; Actinobacteridae; Bifidobacteriales;
Bacteria; Actinobacteria; Actinobacterium.
Rifidobacteriaceae; Bifidobacterium.
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Hypothetical protein.
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                                 Pessi G., Zwahlen M.-C., pridmore R.D., Arigoni F.;
                                                                                                       STRAIN=NCC 2705;
MEDLINE=22294977; PubMed=12381787;
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01-MAR-2003
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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                                                                  Schell M.A., Karmirantzou M.,
Pessi G., Zwahlen M.-C., Desi
                                                                                                                                        SEQUENCE FROM N.A. STRAIN=NCC 2705;
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Pfam; PF02770; Acyl-CoA_dh_M; 1.
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InterPro; IPR006090; Acyl-CoA_dh_C.
InterPro; IPR006091; Acyl-CoA_dh_M.
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GO:0003995; F:acyl-CoA dehydrogenase activity;
GO:0015491; F:oxidoreductase activity; IEA.
genome sequence of Bifidobacterium he human gastrointestinal tract.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41252 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.4%;
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Pred. No.
                                                               Snel B., Vilanova D., E
ere F., Bork P., Delley
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RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
RA Cchillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Feltwell T., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
RA Feltwell S., Morberczak H., O'Neil S., Ormond D., Price C.,
RA Fabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Whitehead S., Barrell B.G., Maskell D.J.;
"Comparative analysis of the genome sequences of Bordetella pertussis, RT Bordetella parapertussis and Bordetella bronchiseptica.";
RT Nat. Genet. 35:32-40(2003).
REMBL, BX640451, CAE34951.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Q7WEP5;
01-OCT-2003
01-OCT-2003
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EMBL; AE014703; AAN24629.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical SEQUENCE 2:
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SEQUENCE
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STRAIN=RB50 / ATCC BAA-588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alcaligenaceae;
NCBI_TaxID=518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                            Q7W3C6 PRELIMINARY; PRT; 273 AA.
Q7W3C6;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                         Bordetella parapertussis.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
     SEQUENCE FROM N.A.
STRAIN=12822 / ATCC BAA-587;
                                                                                                                                                                                                                      Putative enoyl-CoA
                                                                             NCBI_TaxID=519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 ASDDYDSD 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteome.
273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERLHRELA
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212 AA; 25137 MW; EDA495CD83D8B53D CRC64;
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(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                      hydratase.
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C.M., Bentley S.D., Mungall K.L.,
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o. 15;
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RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Achtman M., Hinney A., Temple L., James K., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Chillingworth T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
RA Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squartes R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT (Comparative analysis of the genome sequences of Bordetella pertussis,
RT (Comparative analysis of the genome sequences of Bordetella pertussis,
RT Nat. Genet. 35:32-40(2003).
REMBL, BX440435; CAB39398.1; -.
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RO STRAIN-TO-hama I / ATCC BAA-589 / NCTC 13251;

RO STRAIN-TO-hama I / ATCC BAA-589 / NCTC 13251;

REDLINES-22827954; PubMed=12910271;

REDLINES-22827954; PubMed=12910271;

RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,

RA Parkhill J., Sebaihia M., Preston A., Bentley S.D., Mungall K.L.,

RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

RA Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,

RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

RA Crollingworth T., Collins M., Cronin A., Davis P., Doggett J.,

RA Crollingworth T., Collins M., Cronin A., Davis P., Doggett J.,

RA Crollingworth T., Collins M., Cronin A., Davis P., Doggett J.,

RA Crollingworth T., Collins M., Cronin A., Davis P., Doggett K.,

RA Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

RA Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

RA Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

RA Abdinowitsch E., Rutter S., Sanders D., Seeger K.,

RA Leather S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

RA Sharp S., Simmonds M., Skelton J., Sayares R., Squares S., Stevens K.,

RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,

"Comparative analysis of the genome sequences of Bordetella pertussis,

RT Mat. Genet. 35:32-40(2003).

RT Scrolling R. Cheld 35:69.1; -.

REL Corolling R. Cheld 35:69.1; -.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Alcaligenaceae, Bordetella
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RESULT 11 Q9FNU1 ID Q9FNU1

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RESULT 13
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MEDLINE=21140318; PubMed=11244114;
Dubcovsky J., Ramakrishna W., SanMiguel P.J.,
Shiloff B.A., Bennetzen J.L.;
"Comparative sequence analysis of colinear ba:
artificial chromosomes.";
Plant Physiol. 125:1342-1353(2001).
EMBL; AY013245; AAG45493.1; -.
Gramene; Q9PNU1; -.
SEQUENCE 296 AA; 33226 MW; CC472BACED6776(
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Q8ZZM7;
01-MAR-2002
01-MAR-2002
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01-MAR-2001
01-MAR-2001
01-OCT-2002
  Q9XS63
                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
EMBL; AE009754; AAL62612.1; -.
GO; GO:000166; F:nucleotide binding; IEA.
InterPro; IPR00359; AAA_ATPase.
SMART; SM00382; AAA; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 408 AA; 46291 MW; 02A24E5A2523386F CRC64;
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=IM2 / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792869;
Fitz-Gibbon S.T., Ladner H., Kim U.
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Eukaryota; Viridiplantae;
                                                                                                                                                                                                                   "Genome sequence of the hyperthermophilic crenarchaeon aerophilum."_{i}
                                                                                                                                                                                                                                                                                                          Thermoproteaceae; Pyrobaculum NCBI_TaxID=13773;
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Archaea; Crenarchaeota;
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protein PAE0172.
  PRELIMINARY;
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01-NOV-1999
01-NOV-1999
01-MAR-2003
                                                                                                                                                            STRAIN=cv. Nipponbare;
Buell C.R., Yuan Q., Oyang S., Liu J., Gansberger K., Jones K.M.,
Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
Vanaken S.S., Haed B.J., Suh B.B., Peterson J.J., Quackenbush J.,
White O., Salzberg S.L., Fraser C.M.;
White O., Salzberg S.L., Fraser C.M.;
"Oryza sativa chromosome 3 BAC OJ1112_G08 genomic sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QBILNS;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein OJ1112 G08.17.
OSJNBA0032E21.01 OR OJ1112 G08.17.
Oryza sativa (japonica cultivar group).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Cordonnier-Pratt M.-M.;
"Untitled.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00659; CHROMOGRANIN.
PROSITE; PS00422; GRANINS_1; 1.
PROSITE; PS00423; GRANINS_2; 1.
SEQUENCE 448 AA; 49861 MW; 1
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InterPro; IPR001990; Granin.
Pfam; PF01271; Granin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Equus caballus CgA mRNA for chromogranin
J. Vet. Med. Sci. 62:953-959(2000).
EMBL; AB025570; BAA76748.l; -.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
Submitted (JUN-2003) to the EMBL; AF377947; AAM34395.2;
                                                                 STRAIN=cv.
                                                                                                                                                  Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (MAY-2002) to the
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                                               Buell
                                                                                               SEQUENCE FROM N.A.
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8; Conserv
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Hasegawa T., Katayama Y.,
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                                                                                                                                               (NOV-2002)
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Pred. No.
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RESULT 15
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C STRAIN=MB4 / JCM 11007;

C STRAIN=MB4 / JCM 11007;

X MEDLINE=21992816; PubMed=11997336;

X MEDLINE=21992816; PubMed=11997336;

X MEDLINE=21992816; PubMed=11997336;

X Dang V., Yu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,

A Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Dong X., Ma Y., Ling L.,

A Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,

Tan H., Chen R., Wang J., Yu J., Yang H.;

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Tan H., Chen R., Yu J., Yu J., Yang H.;

Tan H., Chen R., Yu J., Yu 
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.3%; Score 8; DB 16; Length 525; Best Local Similarity 100.0%; Pred. No. 35; Matches 8; Conservative 0; Mismatches 0; Indels
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Hypothetical protein.
SEQUENCE 516 AA; 58268 MW; 0B9B6A77D0273F55 CRC64;
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(BR9U3;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
predicted kinase related to dihydroxyacetone kinase.
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Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
protein - protein search, using sw model
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OM protein - protein search, using sw model

Run on: April 6, 2004, 19:40:52 ; Search time 23 Seconds (without alignments) 1402.880 Million cell updates/sec

Title: US-10-030-829-3 Perfect score: 625

Sequence:

ring table: OLIGO

1 MSSRAGPMSKEKNVQGGYRP......EFDEALEQLMYKHGLHNEDD 625

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size: 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database: Issued Patents AA:*

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	ъ	4.	ω	2	_	Result No.
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375	361	351	312	300	295	288	283	257	257	257	257	257	257	257	233	175	162	108	102	94	94	94	85	521	418	327	Length
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4312,	e 12349,	Sequence 28, Appl	Sequence 31204, A	Sequence 12934, A	5063, A	e 3,	6	e 4,	4.	4,	4	7,	е4,	4,	Sequence 4354, Ap	e 13, Ap	Sequence 22093, A	Seguence 28062, A	7823, A	31,	Sequence 31, Appl	e 31, Ap	e 4934,	5969,	e 872	Sequence 30948, A	Description

7 1.1 395 4 US-09-673-95A-612 7 1.1 445 4 US-09-252-991A-28986 7 1.1 453 4 US-09-711-164-349 7 1.1 454 4 US-09-813-918-2 7 1.1 456 4 US-09-813-918-2 7 1.1 519 4 US-09-522-991A-28608 7 1.1 519 4 US-09-489-039A-11591 7 1.1 528 4 US-09-489-039A-11591 7 1.1 530 3 US-09-180-8806-8 7 1.1 530 4 US-09-252-991A-29652 7 1.1 577 2 US-08-756-317-13 7 1.1 578 3 US-09-756-317-13 7 1.1 578 3 US-09-756-317-13 7 1.1 589 4 US-09-252-991A-26463 7 1.1 630 4 US-09-252-991A-26463 7 1.1 630 4 US-09-252-991A-26463	45	44	43	42	41	40	39	38	37	36	35	34	ω u	32	31	30	29	č
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	US-09-252-991A-26576	US-09-252-991A-19822	US-09-252-991A-26463	US-09-543-681A-6155	US-08-981-215-1	US-08-756-317-13	US-09-252-991A-29652	US-09-356-806-113	US-09-180-852-2	US-09-356-806-8	US-09-489-039A-11591	US-09-252-991A-28608	US-09-543-681A-5516	US-09-813-918-2	US-09-711-164-349	US-09-252-991A-28986	US-09-673-395A-612	00 00 00000
	26576, A	19822, A	26463, A	6155, Ap	1, Appli	13, Appl	29652, A	113, App	2, Appli	8, Appli	11591, A	28608, A	5516, Ap	2, Appli	349, App	28986, A	612, App	

ALIGNMENTS

RESULT 2 US-09-489-039A-8728 Sequence 8728, Application US/09489039A PACENT NO. 6610836 PACENT NO. 6610836 GENERAL INFORMATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS PILE REFERENCE: 2709.2004001 CURRENT APPLICATION NUMBER: US/09/489,039A CURRENT FILING DATE: 2000-01-27 PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR APPLICATION NUMBER: US 60/117,747 PRIOR FILING DATE: 1999-01-29 **UMMBER OF SEQ ID NOS: 14342 **SEQ ID NO 8728 LENGTH: 418 TYPE: PRT **CRGANISM: Klebsiella pneumoniae**	Query Match 1.3%; Score 8; DB 4; Length 327; Best Local Similarity 100.0%; Pred. No. 17; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 109 GRGRALSR 116 Db 113 GRGRALSR 120	CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 PRIOR FILING DATE: 1998-07-27 PUBBER OF SEQ ID NOS: 33142 SEQ ID NO 30948 LENGTH: 327 TYPE: PRT ORGANISM: Pseudomonas aeruginosa US-09-252-991A-30948	RESULT 1 US-09-252-991A-30948 US-09-252-991A, Application US/09252991A ; Sequence 30948, Application US/09252991A ; Patent No. 6551795 ; GENERAL INFORMATION: ; APPLICANT: Marc J. Rubenfield et al. ; APPLICANT: Marc J. Rubenfield et al. ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS ; FILE REFERENCE: 107108
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RESULT 3
US-09-543-681A-5969
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              US-08-629-291A-31
; Sequence 31, Application US/08629291A
; Patent No. 5959174
                                                                                                                                                                   Query Match
Best Local Similarity
Thes 7; Conserve
                                                               RESULT 5
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Best Local Similarity
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SEQ ID NO 5969
LENGTH: 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4934, Application US/09543681A Patent No. 6605709
                                                                                                                                                                                                                                                                                                  SEQ ID NO 4934
LENGTH: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/543,61
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FILS REFERENCE: 2709.1002-001
                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 2709.1002-001 (CURRENT APPLICATION NUMBER: US/09/543,681A CURRENT FILING DATE: 2000-04-05 PRIOR APPLICATION NUMBER: US 60/128,706 PRIOR FILING DATE: 1999-04-09 NUMBER OF SEQ ID NOS: 8344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 1.3%; Sometime 1.3%; Sometime 100.0%; les 8; Conservative 0;
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                                                                                                                                               470 EIMSEKL 476
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                                                                                                                 13 EIMSEKL 19
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                                                                                                                                                                               1.1%; Score 7; DB 4 ilarity 100.0%; Pred. No. 53; Conservative 0; Mismatches
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k; Pred. No. 25;
0; Mismatches
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o. 21;
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o. 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                      COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn palane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                               CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                               COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                             STREET:
              APPLICATION NUMBER:
                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                 E: Pennie & Edmonds
1155 Avenue of the Americas
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US/08/658,335B

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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 94 amino
                                                                                                                 Sequence 31, Application US/08658335B Patent No. 5981703
                                                                                                   GENERAL INFORMATION:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
COURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/629,291A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 59
TELECOMMUNICATION INFORMATION
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION:
APPLICANT: Hsieh, Ming-Hsiun
TITLE OF INVENTION: PLANT GLUTAMATE RECEPTORS
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 08-APR
                                                                                                                                                                                                                                                                               Local Similarity les 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                         543 QNINPSS 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /AGENT INFO...
Coruzzi, Laura A.
Coruzzi, Taura A.
coruzzi, 10,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1: Pennie & Edmonds
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                               1.1%; imilarity 100.0%; Conservative 0
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Lam, Hon-Ming
Hsieh, Ming-Hsuin
VENTION: PLANT GLUTAMATE RECEPTORS
EQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coruzzi, Gloria
                                                    Oliveira, Igor
Lam, Hon-Ming
                                                                                   Coruzzi, Gloria
                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                  single
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                                                                                                                                                                                                                                                                                      ; Score 7; DB 2
%; Pred. No. 57;
0; Mismatches
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Gaps

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FILING DATE: 0. CLASSIFICATION:

05-JUN-1996

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US-09-406-640-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 31, Application US/09406640 Patent No. 6451546 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                        TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: COTUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 5914-052
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Coruzzi, Laura A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 1.1%; Score 7; DB Local Similarity 100.0%; Pred. No. 57 les 7; Conservative 0; Mismatches
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
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                                                                                                                                                                                                             NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 5914-082
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-990
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/406,640
PILING DATE: 27-Sep-1999
CLASSIFICATION: -Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
            TOPOLOGY: linear MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: S
                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Coruzzi, Gloria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 QNINPSS 70
                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                               LENGTH: 94 amino acids
                                                                                                                                                                                                TELEFAX: (212) 869-9741/8864
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Lam, Hon-Ming
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                 SEQ ID NO: 31:
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                                                                                                                                              US-09-252-991A-28062
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                                                                                    Query Match
Best Local S
                                                                                                                                                                                               PRIOR FILING DATE: 1:
NUMBER OF SEQ ID NOS:
SEQ ID NO 28062
LENGTH: 108
                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: MAIC J. Rubenfield et al.
APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28062, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
SEQ ID NO 7823
                                                                       Matches
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Matches 7; Conserv
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Matches 7; Conserv
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILITITE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-0
                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 102
TYPE: PRT
ORGANISM: Proteus mirabilis
                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     543 QNINPSS 549
                                   141 ARGGSAQ 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 KLHRELA 265
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42 ARGGSAQ 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 KLHRELA 65
                                                                     Similarity 7; Conserv
                                                                       Conservative
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                                                                                                                                                                                                                                                                                    UMBER: US 60/074,788
1998-02-18
                                                               100.0%; ++
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100.0%; Pred. No. 57;
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100.0%; Pred. No.
                                                                     1.1%; Score 7; DB .
100.0%; Pred. No. 64
ive 0; Mismatches
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o. 61;
                                                                                                       Length 108;
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                                                                       Indels
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TRESULT 10 US-09-152-991A-22093 ; Sequence 22093, Application US/09252991A ; Patent No. 6551795 0

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CURRENT APPLICATION NUMBER: US/09/705,621
CURRENT FILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PRICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 22093
LENGTH: 162
TYPE: PRI
DENIFORMER OF SERVICIONAS ABENUGIOSA
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US-09-252-991A-22093
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patent No. 6673355
GENERAL INFORMATION:
APPLICANT: ESTES, MARY
TITLE OF INVENTION: ROT
FILE REFERENCE: P01932U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-705-621-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
ORGANISM: Proteus mirabilis
US-09-543-681A-4354
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                                                GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: GARY BRETON

APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: USAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: USAGNOSTICS AND THERAPEUTICS

TITLE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

CURRENT FILING DATE: 2000-04-05

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 4354

LENGTH: 233

THERAPEUTICS

LENGTH: 233
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Best Local &
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ITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
ITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                           Sequence 4354, App
Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Rotavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity les 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.0%; Pies 7; Conservative 0;
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100.0%; Pred. No. 90)
tive 0; Mismatches
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US-08-451-947-4
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Best Local S
Matches 7
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                                                                                                          US-08-451-947-4
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                                                                                                                                                                                                                                                                                                                                       FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648
FILING DATE: 31-JAN
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426
FILING DATE: 19-APR-1995
PRIOR APPLICATION UMBER: 08/030
APPLICATION NUMBER: 08/030
                                                     Matches
                                                                  Query Match
Best Local 9
                                                                                                                                                                                  TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 4:
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TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
NUMBER OF SEQUENCES: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
118/08/4
                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                   FILING DATE: 1991
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 66
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/587707
                                                                                                                                                                                                              TELEFAX:
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7; Conserva
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                            452 KNKLSKQ 458
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                                                                         Similarity
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   KNKLSKQ 51
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SYSTEM: PC-DOS/MS-DOS
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                                                         Conservative
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                                                                       1.1%;
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                                                               Mismatches
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5. 1.2e+02;
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                                                                                            Length 257;
                                                                     Indels
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RESULT 14 US-08-424-826A-4

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Sequence 4, Application US/08424826A

GENERAL INFORMATION:

APPLICANT: Rosenthal, Arnon IIILE OF INVENTION: NOVEL N

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RESULT 15
US-08-910-691-7
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Best Local Similarity
7; Conserv
                                                                                                                                                                                                                                                        Sequence 7, Application US/08910691 Patent No. 6015552
                                                                                                          GENERAL INFORMATION:
APPLICANT: WATANABE, Tatsuya
APPLICANT: YOSHITOMI, Sumie
APPLICANT: SASADA, Reiko
TITLE OF INVENTION: THERAPEUTIC AGENT FOR NEUTROPENIA
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 08/240387
APPLICATION NUMBER: 08/240387
FILING DATE: 10-May-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648482
PRIOR APPLICATION NUMBER: 07/587707
PRILING DATE: 31-JAN-1991
PRIOR APPLICATION NUMBER: 07/587707
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REPERENCE/DOCKET NUMBER: 90666P1C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TRILEPAY: 415/25-8067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOPTWARE: WinPatin (General CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 19-Apr-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STATE: N
COUNTRY:
                                                     ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 257 amin
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                       CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                              452 KNKLSKQ 458
                                                                                                                                                                                                                                                                                                                                                                           45 KNKLSKQ 51
  Massachusetts
7: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/424,826A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 7; ; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Ler
Jo. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Query Match
Best Local Similarity
Watches 7; Conserve
밁
                                                                                                                                             ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-910-691-7
                                                                                                                                                                                                                                      NAME: NEUNER, George W
REGISTRATION NUMBER: 26964
REFERENCE/DOCKET NUMBER: 1234:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEPAX: (617)523-6440
TELEPAX: (617)523-6440
TELEPAX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,691
FILING DATE:
CTRECTORY
                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/01
APPLICATION NUMBER: US/01
FILING DATE: 19930604
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                       ENGTH:
                     452 KNKLSKQ 458
45 KNKLSKO 51
                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                         257 amino acids
                                                                         Conservative
                                                                     1.1%; Score 7; DB 3; Len
100.0%; Pred. No. 1.3e+02;
ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/074,969
                                                                                                                                                                                                                                                                                                                                                          12345
                                                                                                      Length 257;
                                                                         Indels
                                                                       0,
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Search completed: April 6, 2004, 19:44:36 Job time : 24 secs

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Minimum DB
Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          April 6, 2004, 19:43:32; Search time 46 Seconds (without alignments) 3568.388 Million cell updates/sec
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625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MSSRAGPMSKEKNVQGGYRP......EFDEALEQLMYKHGLHNEDD 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                       cgn2_6/ptodata/1/pubpaa/USO:
cgn2_6/ptodata/1/pubpaa/PCT
m2_6/ptodatea/1/pubpaa/US09B_PUBCOMB.pep:*
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_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
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                                                                                                                                                                                                                                                                                                                                     6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                    PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

15	14	13	12	11	10	9	8	7	6	ຫ	4	ω	Ν	1	Result No.
7	7	7	7	7	7	7	7	7	8	9	9	9	. 9	9	Score
1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.3	1.4	1.4	1.4	1.4	1.4	Query Match Length
68	62	60	57	56	56	36	36	18	916	611	382	324	227	223	Length
12	12	12	15	14	12	10	ø	14	12	12	15	12	9	12	DB
US-10-424-599-169910	US-10-424-599-228124	US-10-424-599-154923	US-10-264-049-3845	US-10-029-386-31679	US-10-424-599-250491	US-09-963-693-225	US-09-205-658-225	US-10-225-567A-1514	US-10-282-122A-51413	US-10-425-114-58390	US-10-369-493-12141	US-10-424-599-234018	US-09-738-626-5288	US-10-424-599-234019	ID
Sequence 169910,	Sequence 228124,	Sequence 154923,	Sequence 3845, Ap	Sequence 31679, A	Sequence 250491,	Sequence 225, App	Sequence 225, App	Sequence 1514, Ap	Sequence 51413; A	Sequence 58390, A	Sequence 12141, A	Sequence 234018,	Sequence 5288, Ap	Sequence 234019,	Description

RESULT 2 US-09-738-626-5288

44 U	44	43	42	41	40	39		37		35		ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20	19	. 18	17	16
7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1	1.1
257	257	257	253	227	226	219	216	211	196	189	180	173	166	148	141	139	139	138	138	138	136	136	121	104	104	104	94	78	69
10	10	œ	14	12	12	2	9	12	12	12	12	12	12	15	12	14	14	14	14	12	12	22	15	15	14	9	14	12	14
US-09-788-188-6	US-09-788-188-5	US-08-450-842-4	US-10-029-386-32003	US-10-335-977-5665	US-10-335-977-5666	US-10-282-122A-69066	US-09+861-451A-26	US-10-627-476-128	US-10-425-114-64832	US-10-424-599-283874	-10	US-10-424-599-277920	US-10-425-114-72748	-10	US-10-282-122A-51842	US-10-155-886-57	US-10-155-886-55	US-10-155-886-59	US-10-155-886-53	US-10-424-599-177015	US-10-425-114-69428	US-10-425-114-56375	US-10-108-260A-4862	US-10-227-577-650	US-10-091-504-650	US-09-764-869-650	US-10-223-047-31	US-10-424-599-280255	US-10-106-698-5320
Sequence 6, Appli	n v		w	5665,		e 69	26, A	Sequence 128, App		Sequence 283874,		Sequence 277920,	Sequence 72748, A		5184	57,	55,	•	Sequence 53, Appl		Sequence 69428, A	Sequence 56375, A	4862,	Sequence 650, App	e 650,	_	e 31,		Sequence 5320, Ap

ALIGNMENTS

US-10-424-599-234019

Sequence 5288, Application US/09738626 Publication No. US20020197605A1

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FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
CURRENT FILING DATE: 2000-12-16
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-424-599-234018
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                                                                                                                                                 US-10-424-599-234018
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Best Local Similarity 100.0%;
Matches 9; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 5288
LENGTH: 227
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
S-09-738-626-5288
                                                                                                                                                                                                                       APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: US/10/424,599
TILE REFERENCE: 38-21(5)223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 234018
LENGTH: 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 234018, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                        Matches
                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                   FEATURE: OTHER INFORMATION: Clone ID: PAT_MRT3847_53342C.1.pep
                                                                                                                                                                                                         ORGANISM: Glycine max
                                                                  Local Similarity es 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 DSDALDDSD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 DSDALDDSD 187
119
                                    224 ROWHCPACQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YOKOI, HARUHIKO
TATEISHI, NAOKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IKEDA, MASATO
ROWHCPACO 127
                                                                        ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.4%; Score 9; DB 100.0%; Pred. No. 3. ive 0; Mismatches
                                                                                                Score 9;
                                                                                Mismatches
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o. 3.7;
                                                                                                      DB 12;
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                                                                                  0
                                                                                                                      Length 324;
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RESULT 4

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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TILLE REPERENCE: 38-10(52052)B
FULL REPERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILLNG DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US/0/360,039
PRIOR APPLICATION NUMBER: US/0/360,039
PRIOR APPLICATION NUMBER: US/0/360,039
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-369-493-12141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Mesorhizobium loti
US-10-369-493-12141
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                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3079-030-A8_FLI.pep
US-10-425-114-58390
                                                                                                                                                                                                       밁
                                                                                                             US-10-282-122A-51413
                                                                                                                                     RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 58390, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 58390
LENGTH: 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         equence 12141, Application US/10369493
ublication No. US20030233675A1
ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   1.4%;
Best Local Similarity 100.0%;
Matches 9; Conservative
                                                               Sequence 51413, Application US/10282122A publication No. US20040029129A1
                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Liu, Jingdong APPLICANT: Zhou, Yihua
APPLICANT: Wang, Liangsu APPLICANT: Zamudio, Carlos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 HRELAEVLE 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 HRELAEVLE 24
                                                                                                                                                                                                       218 NGPGAIDWY 226
                                                                                                                                                                                                                                                   233 NGPGAIDWY 241
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                                                                                                                                                                                                                                                                                                                            Score 9; DB 12; Length 611; Pred. No. 8.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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Malone, Cheryl

US-10-225-567A-1514

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APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
APPLICANT: ROUSH, Christine L.
TITLE OF INVENTION: ANTIGERIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT PAPLICATION NUMBER: US/10/225,567A
CURRENT APPLICATION NUMBER: 60/257,144
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patentin version 3.1
SEQ ID NO 1514
LERGTH: 18
TYPE: PRT
ORGANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-282-122A-51413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1
SEQ ID NO 51413
LENGTH: 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
CURRENT FILING UNUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
RRIOR APPLICATION NUMBER: 60/230,335
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FITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-2
APPLICATION NUMBER: 60/267,636
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Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trawick, John
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o. 1.2e+02
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APPLICANT: RUYKNI, GARY
APPLICANT: Ogg. Scott
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/351004
CURRENT APPLICATION NUMBER: US/09/205,658
CURRENT FILING DATE: 1998-12-03
EARLIER APPLICATION NUMBER: 08/857,076
EARLIER APPLICATION NUMBER: 08/88,534
EARLIER APPLICATION NUMBER: 08/88,534
EARLIER APPLICATION NUMBER: US98/10080
EARLIER APPLICATION NUMBER: US98/10080
EARLIER APPLICATION NUMBER: US98/10080
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US-09-205-658-225
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; ORGANISM: Caenorhabditis elegans
US-09-963-693-225
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                                                               NUMBER OF SEQ ID NOS: 328
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 225
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 225, Application US/09963693
Publication No. US20030181364A1
GENERAL INFORMATION:
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SEQ ID NO 225
LENGTH: 36
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Best Local
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Best Local Similarity
                                                                                                                                                                          PRIOR APPLICATION NUMBER: US/09/205,658
PRIOR FILING DATE: 1998-12-03
PRIOR APPLICATION NUMBER: 08/857,076
PRIOR FILING DATE: 1997-05-15
PRIOR APPLICATION NUMBER: 08/888,534
PRIOR FILING DATE: 1997-07-07
PRIOR APPLICATION NUMBER: US98/10080
                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/963,693
CURRENT FILING DATE: 2001-09-25
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ruvkun, Gary
APPLICANT: Ogg, Scott
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/351004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                       PRIOR FILING DATE: 1998-05-15
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b. US20010029617A1
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RESULT 10
US-10-424-599-250491
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Best Local Similarity
Matches 7; Conserv
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                                                                          OTHER INFORMATION: MAP TO AC008974.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.87
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.55
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.8
OTHER INFORMATION: SWISSPROT HIT: Q00535, EVALUE 2.80e+00
US-10-029-386-31679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 250491, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(5323)B CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 31679, Application US/10029386 publication No. US20030194704A1
                                                                                                                                                                                                                                                     SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 31679
LENGTH: 56
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                                                                                                                                                                                                                                                                                                         APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HANZEL, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
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                                       Query Match
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TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100
les 7; Conservative
1.1%; Score 7; DB 14; Length 56;
Local Similarity 100.0%; Pred. No. 1e+02;
hes 7; Conservative 0; Mismatches 0; Indels
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ilarity 100.0%;
Conservative (
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100.0%; Pred. No. 1e+02;
rative 0; Mismatches 0; Indels
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0; Mismatches
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o. 69;
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                    Gaps
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SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 3845
LENGTH: 57
TYPE: PRT
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US-10-264-049-3845
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; NAME/KEY: MISC_FEATURE
; LOCATION: (1)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino US-10-264-049-3845
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Publication No. US20
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-424-599-154923
                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT3847_110917C.1.pep US-10-424-599-154923
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kovalic David K

APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
FULE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 154923
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Best Local S
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FILE REFERENCE: PA13391
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR PILING DATE: 2001-06-07
PRIOR PILING DATE: 2000-06-07
PRIOR PILING DATE: 2000-06-07
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          RESULT 14
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Best Local (
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7; Conservative
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. US20040005579A1
                                                                                                            EVECLVQ 27
                                                                                                                                                 Conservative
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0; Mismatches
                                                                                                                                                     Score 7; DB 12; L; Pred. No. 1.1e+02; 0; Mismatches 0;
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lo. 1e+02;
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Length 60 Indels

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Matches

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NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 169910
LENGTH: 68
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
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US-guence 228124, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
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US-10-424-599-169910
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Search completed: April 6, 2004, 19:49:22
Job time : 47 secs
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                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: PAT_MRT3847_124443C.1.pep
US-10-424-599-169910
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Best Local S
Matches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 228124
LENGTH: 62
TYPE: PRT
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Best Local S
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)8
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
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APPLICANT: Kovalic David K
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FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(62)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                          / Match 1.1%; Score 7; DB 12; Length 68;
Local Similarity 100.0%; Pred. No. 1.2e+02;
les 7; Conservative 0; Mismatches 0; Indels
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Local Similarity 100.0%; P
nes 7; Conservative 0;
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                                                                                                                                 561 SSFIEFQ 567
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                                                                                      22 SSFIEFQ 28
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